GRVER51.SEQ ATGATGAAACGCGAAAAGAACGTGATCTACGGCCCAGAAC	40
GR6. SEQ ATGATGAAA CGCGAAAAAGAACGTGATCTACGGCCCAGAAC	40
GRVER5. SEQ ATGATGAAA CGCGAAAAAGAACGTGATCTACGGCCCAGAAC	40
GRVER4.SEQ ATGATGAAAAGAAAGAACGTGATCTACGGCCCAGAAC	40
GRVER3. SEQ ATGATGAA A CGC GAAAAAG A A CGT GATC TA CGG CC CA GAAC	40
GRVER2.SEQ ATGATGAAA CGCGAAAAAGAACGTCATCTACGGCCCAGAGA	40
GRVER1.SEQ ATGATGAAACGGAAAAGAACGTCATCTACGGCCCAGAGC	40
YG81-6G1. SEQATGATGAAGCGAGAGAAAAATGTTATATATGGACCCGAAC	40
RDVER1.SEQ ATGATGAAGCGTGAGAAAAATGTGATTATGGTCCTGAAC	40
RDVER2.SEQ ATGATGAAGCG T GAGAAAATGT G AT T ATGG T CC T GAAC	40
	40
	40
RDVER5.SEQ ATGATGAAGCGTGAGAAAATGTCTATGGCCCTGAGC	40
	40
	40
RDVER52.SEQ ATGATGAAGCGTGAAAAAATGTCATCTATGGCCCTGAAGC	40
RD1561H9.SEQATGATAAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGC	40
GRVER51.SEQ CACTGCATCCACTGGAAGACCTCACCGCTGGTGAGATGCT	80
GR6.SEQ CACTGCATCCACTGGAAGACCTCACCGCTGGTGAGATGCT	80
GRVER5. SEQ CACTGCATCCACTGGAAGACCTCACCGCTGGTGAGATGCT	80
GRVER4. SEQ CACTGCATCCACTGGAAGACCTCACCGCTGGTGAGATGCT	80
GRVER3. SEQ CACTGCATCCACTGGAAGACCTCACCGCTGGTGAGATGCT	80
GRVER2. SEQ CITCTGCACCCATTGGAAGACCTGACCGCTGGTGAGATGTT	80
GRVER1. SEQ CTCTGCACCCATTGGAAGACCTGACCGCCGGTGAGATGTT	80
YG81-6G1.SEQC C C T A C A C C C C T T G G A A G A C T T A A C A G C T G G A G A A T G C T	80
RDVER1.SEQ CATTGCATCCTCGGAGGATTTTGACTGCTGCCGGAAATGCT	80
RDVER2.SEQ CATTGCATCCTCTGGAGGATTTTGACTGCCGGCGAAATGCT	80
RDVER3.SEQ CITTIGCACCCITTIGGAGGATTTTGACTGCCGGCGAAATGCT	80
RDVER4.SEQ CITITGCATCCTTTGGAGGATTTTGACTGCCGGCGAAATGCT	80
RDVER5. SEQ C T CTC CA T CC T TTGGA G GA T TT G AC T GC C GG C GAAATGCT	80
RD7.SEQ C T CTC CA T CC T TTGGA G GA T TT G AC T GC C GG C GAAATGCT	80
RDVER51.SEQ C T CT CA T CC T TTGGA GGA T TT GAC T GC C GG CGAAATGCT	80
RDVER52.SEQ CITIC T C C A T C C T T T G G A G G A T T T T G A C T G C C G G C G A A T G C T	80
RD1561H9. SEQCICTIC AICCITTIGGA GGAITTIGA CIGCIGGIGA A AIGCI	80
	120
GR6.SEQ CTTCCGAGCTGCGTAAACATAGTCACCTCCCTCAAGCA	120
	120
	120
GRVER3.SEQ GTTCCGTGCCCTGCGTAAACATAGCCACCTGCCTCAAGCT	120
GRVER2.SEQ GTT C C G T G C T C T G C G T A A A C A T T C T C A C T T G C C T C A A G C C GRVER1.SEQ GTT C C G T G C T C T G C G T A A A C A T T C T C A C T T G C C T C A A G C C	120
	120
	120
	120
	120
	120
	120
* 1 - 1 1 - 1 - 1 1 1 1	120
- 1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1	120
	120
	120
	120

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GRVER51.SEQ CITCG TGG MCGTCG TGG GAG A C G A G A G C C TCT C C T A C A A A G 160
         CTCGTGGACGTCGTGGGAGACGAGAACCTCTCCTACAAAG 160
GR6.SEO
        CTCGTGGACGTCGTGGGAGACGAGAGCCTCTCCTACAAAG 160
GRVER5.SEQ
         CTCGTGGACGTCGTGGGAGACGAGAGCCTCTCTTACAAAG 160
GRVER4.SEQ
GRVER3.SEO
         CTCGTGGACGTCGTGGGTGACGAGAGCCTGTCTTACAAAG 160
GRVER2.SEO
        CTGGTCGATGTCGTGGGCGACGAGAGCTTGTCTTATAAGG 160
GRUERL. SEQ CTGG TGG AT GTCG TGG G C G A C G A A G C TT GT CTT A T A A G G 160
YG81-6G1. SEQTTAGTAGATGTGGTTGGCGACGAATCGCTTTCCTATAAAG 160
RDVER1.SEQ TTGGTCGACGTGGTCGGTGATGAGTCTCTGAGCTACAAAG 160
RDVER2.SEQ TTGGTGGACGTGGTCGGTGATGAATCTCTGAGCTACAAAG 160
RDVER3.SEQ TTGGTCGATGTGGTCGGCGATGAATCTTTGAGCTATAAGG 160
RDVER4.SEQ TTGGTCGATGTGGTCGGCGATGAATCTTTGAGCTACAAGG 160
ROVERS-SEQ TTGGTTCGATGGGTCGGCGATGAATCTTTGAGCTACAAGG160
RD7.SEQ TTGGTTCGATGGTCGGCGATGAATCTTTTGAGCTACAAGG160
RD7.SEQ TTGGTTCGATGGTCGGCGATGAATCTTTTGAGCTACAAGG160
ROVERS5.SEQ TTGGTCGATGTGGTCGGCGATGAATCTTTTGAGCTACAAGG160
RD1561H9.SEQT TGGTCGATGTGGTCGGCGATGAATCTTTGAGCTACAAGG 160
GRVERSI.SEQ AATTTTTCGAAGCTACTGTGCTGCTGTTGGCCCAAAGCCTCCA 200
GR6.SEQ AATTTTTCGAAGCTACTGTGCTGTTGGCCCAAAGCCTCCA 200
GRVERS. SEQ. A A T T T T T C G A A G C T A C T G T G C T G T T T G G C C C A A A G C C T C C A 200
GRVER4.SEQ A A T T T T T C G A A G C T A C T G T G C T G T T T G G C C C A A G G C T C C A 200
GRVER3.SEQ AATTTTTCGAAGCTACTGTCCTGTTTGGCCAAAGCCTGCA200
GRVER2.SEQ AATTTTTCGAAGCTACTGTCCTGTTTGGCCCAATCTCTGCA 200
YG81-6G1. SEQAGTTTTTTGAAGCGACAGTCCTCCTAGCGCAAAGTCTCCA 200
RDVER1.SEQ AAT TOTTTGAGGCCACCGTGTTGCTGGCTCAAAGCTTGCA200
RDVER2. SEQ AGTTCTTTGAGGCAAACCGTGTTGCTGGCTCAGAGCTTGCA 200
RDVER3.SEQ AGTTTTTTGAGGCAACCGTCTTGCTGGCTCAGTCTTTGCA 200
RDVER4.SEQ AGTTTTTTGAGGCAACCGTCTTGCTGGCTCAGTCCTTGCA
RDVER5.SEQ AGTTTTTTGAGGCAACCGTCTTGCTGGCTCAGTCCCTCCA 200
RDVER51. SEQ AGTTTTTTGAGGCAACCCGTCTTTGCTGGCTCAGTCCCTCCA 200
RDVER52. SEQ AGTTTTTTGAGGCAACCGTCTTGCTGGCTCAGTCCCTCCA 200
RD1561H9. SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A 200
GRVER51. SEQ TAATTGTGGGTACAAAATGAACGATGTGGTGAGCATTTTGT 240
GR6.SEQ
        ITIA A T T G T G GIGIT A C A AIAIA T G A AICIG A T G T IGIG T GIA G CIA TITIT GITI 240
GRVER5. SEQ TAATTGTGGGTACAAAATGAACGATGTGGTGAGCATTTGTZ40
GRVER4. SEQ TAATTGTGGATACAAAAATGAACGATGTGGTGAGCATTTTGT 240
GRVER3.SEQ TAATTGTGGTTACAAAATGAACGATGTGGTGAGCATCTGT 240
GRVER2. SEQ TAATTGCGGTTACAAAATGAACGATGTGGTCAGCATTTTGT 240
GRVER1. SEQ TAATT GCG GTTACAAAATGAACGATGTGGTCAGCATTTTGT 240
YG81-6G1.SEQC A A T T G T G G A T A C A A G A T G A A T G A T G T A G T G T C G A T C T G C 240
RDVER1.SEQ CAACTGTGGCTATAAGATGAATGACGTCGTGTCTATCTGC 240
RDVERZ. SEQ CAACTGTGGCTATAAGATGAATGACGTCGTGTCTATCTGC 240
RDVER3. SEQ TAATTGGGGCTACAAGATGAACGACGTCGTCTTATTTGT 240
RDVER4. SEQ TAATTGTGGCTACAAGATGAACGACGTCGTCTCCATTTGTC1240
RDVER5.SEQ CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGT 240
        CAATTGTGGCTACAAGATGAACGTCGTCGTTAGTATCTGT 240
RDVER51.SEQ CAATTGTGGCTACAAGATGAACGTCGTTAGTATCTGT 240
RDVER52. SEQ CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGT 240
RD1561H9. SEQC A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T 240
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FIG. 2 (cont'd)

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GRVER51. SEQ G C T G A G A A T A A C A C T C G C T T C T T T A T T C C T G T A A T C G C T G 280
GR6.SEO
               GCTGAGATAACACTCGCTTCTTTTTTCCTGTAATCGCTG 280
GRVERS. SEQ G C T G A G A A T A A C A C T C G C T T T T T T T C C T G T A A T C G C T G 280
GRVER4.SEQ GCTGAGAATAACACTCGCTTCTTTATCCCTTATCGCTG 280
GRVER3.SEQ GCTGAGAATAACACTCGCTTTTTTTATCCCTTGTGATCGCTG 280
GRVER2. SEQ G C T G A G A A T A A C A C C C G C T T T T T C A T C C C A G T G A T T G C C G 280
GRVER1.SEQ GCTGAGAATAACACCCGCTTTTTCATCCCGAGTGATTGCCG 280
YG81-6G1. SEQG C C G A G A A T A A T A C A A G A T T T T T T T T T C C C G T T A T T G C A G 280
RDVER1.SEQ GCCGAAAACAATACTCGTTTCTTTATTCCTGTCATCGCTG 280
RDVERZ.SEQ G C C G A A A A C A A T A C T C G T T T T C T T T A T T C C T G T C A T C G C G Z 280 RDVERZ.SEQ G C C G A A A A C C A A T A C C C G T T T T C T T C A T T C C A G T C A T C G C G Z 280
RDVER4. SEQ G CAGA A A A CA A TA CC CGTTTTCTTCATTCCAGTCATCGCCG 280
RDVER5.SEQ GCTGAAAACAATACCCGGTTTTCATTCATTCCAGTCATCCAGCCG 280
               GCTGAAAACAATACCCGTTTTCTTCATTCCAGTCATCGCCG 280
RDVER51. SEQ G C T G A A A A C A A T A C C C G T T T T C T T C A T T C C A G T C A T C C G C C G 280
RDVER52. SEQ G C T G A A A A C A A T A C C C G T T T C T T C A T T C C A G T C A T C G C C G 280
RD1561H9. SEQG CTG AAAACAATACCCGTTTTCTTCATTCCAGTCATCGCCG 280
GRVER51.SEQ CTTGGTACATCGGCATGATTGTCGCCCCTGTGAATGAATC
GR6.SEO
               CTTGGTACATCGGCATGATTGTCGCCCCTGTGAATGAATC
GRVERS. SEQ CTTGGTA CATC GGC ATGATTGT CGC CCTGT GATTGATTG ATTGT CGC CTGT CATGATTGATTGT CGC CTGT CGC ATGATTGT CGC CTGT CGC CT
GRVER4.SEQ CTTGGTACATCGGCATGATTGTCGCCCTGTGAATGAATC 320
GRVER3.SEQ CTTGGTACATCGGCATGATTGTCGCCCTGTGAATGAATC 320
GRVER2.SEQ CTTGGTACATCGGCATGATTGTCGCCCTGTGAATGAATC 320
GRVER1.SEQ CTTGGTACATCGGCATGATTGTCGCCCTGTGAATGAATC 320
YG81-6G1. SEQC T T G G T A T A T T G G T A T G A T T G T A G C A C C T G T T A A T G A A A G 320
RDVER1.SEQ CCTGGTATATTGGTATGATCGTGGCTCCAGTCAACGAGAG 320
RDVER2.SEQ CICITGGTATATTGGTATGATICIGTIGIGCITIC CAIGTICIA AICIGAIGIAG 320
RDVER3. SEQ CCTGGTATATCGGTATGATCGTGGCTCCAGTCAACGAGAG 320
RDVERS. SEQ CATGGTATATCGGTATGATCGTGGCTCCAGTCAACGAGAG 320
RD7.SEQ
              CATGGTATATICIGGTATGATICIGTIGIGCITIC CAIGTICIA AICIGAIGIA G 320
RDVER51. SEQ CATGGTATATCGGTATGATCGTGGCTCCAGTCAACGAGAG 320
RDVER52.SEQ CATGGTATATCGGTATGATCGTGGCTCCAGTCAACGAGAG 320
RD1561H9.SEQCATGGTATATCGGTATGATCGTGGCTCCAGTCAACGAGAG 320
GRVER51.SEQ TTACATCCCAGATGAGCTGTGTGTAAGGTTATGGGTATTAGC 360
GR6.SEQ TTACATCCCAGATGAGCTGTGTGAAGGTTATGGGTATTAGC 360
GRVER5. SEQ TTACATCCCAGATGA GC TG TG TAAGGT TATGGGTAT TAGC 360
GRVER4.SEQ TTACATCCCAGATGAGCTGTGTGTAAGGTTATGGGTATTAGC 360
GRVER3.SEQ TTACATCCCAGATGAGTTGTGTGTAAGGTGATGGGTATTAGC 360
GRVER2.SEQ TTATATCCCAGACGAGTTGTGCAAGGTCATGGGTATTAGC 360
GRVER1.SEQ TTATATCCCAGACGAGTTGTGCAAGGTCATGGGTATTAGC 360
YG81-6G1.SEQTTACATCCCAGATGAACTCTGTAAGGTGATGGGTATATCG 360
RDVER1.SEQ CTACATTCCTGATGAACTGTGTAAAGTGATGGGCATCTCT 360
             CTACATTCCTGATGAACTGTGTAAAGTGATGGGCATCTCT 360
RDVER2.SEQ
RDVER3.SEQ CTACATTCCTGACGAACTGTGTAAAGTCATGGGTATCTCTT 360
RDVER4.SEQ CTACATTCCCGACGAACTGTGTAAAGTCATGGGTATCTCTT 360
              CTACATTCCCGACGAACTGTGTAAAGTCATGGGTATCTCT 360
RDVER5.SEQ
RD7.SEQ
              CITACATITIC CICIGAICIGAACTIGIT GTAAIAIGTICIAT GGGTATICIT CITI 360
RDVER51.SEQ CT A C A TTC CCG ACG A A C TGT G T A A A G T CA T G G G T A T CT CT
RDVER52. SEQ CT A CATTCCCGGACGAACTGTGTAAAAGTCATGGGTATCTCT CT 360
RD1561H9.SEQCITACATICCCGACGAACTGTGTAAAGTCATGGGTATCTCII 360
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FIG. 2 (cont'd)

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GRVER51. SEQ A A A C CT C A A A T C G T C T T T A C T A C C A A A A C A T C T T G A A T A 400
        AAACCTCAAATCGTCTTTACTACCAAAAACATCTTGAATA 400
GR6.SEO
        AAACCTCAAATCGTCTTTACTACCAAAAACATCTTGAATA 400
GRVER5.SEQ
        AAACCTCAAATCGTCTTTACTACCAAAAATATCCTGAATA 400
GRVER4.SEQ
GRVER3.SEQ AAACCTCAAATCGTCTTTACTACCAAAAACATCCTGAATA 400
        AAACCTCAAATCGTGTTTACTACCAAGAACATTCTGAATA 400
GRVER2.SEO
        AAACCTCAAATCGTGTTTACTACCAAGAACATTCTGAATA 400
GRVER1.SEQ
YGB1-6G1.SEQAAACCACAAATAGTTTTTACGACAAAGAACATTTTAAATA 400
RDVER1.SEQ A AGC CACAGATTGTCTTCACCACTAAAAATATCTTGAACA 400
        AAGCCACAGATTGTCTTCACCACTAAAAATATCTTGAACA 400
RDVER2.SEO
        AAGCCACAGATITGTGTTCACCACITAAGAATATTTTGAACA 400
RDVER3.SEQ
RDVER4.SEQ A A G C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A 400
        AAGCCACAGATTGTCTTCACCACTAAGAATATTCTGAACA
RDVER5.SEO
        AAIGIC CACAGATITIG TICIT TICIA CICIA CITIA A GAAITIAT TICITIGIA AICIA 400
RD7.SEO
ROVER51.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A 400
RDVER52.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A 400
RD1561H9.SEQA AGCCACAGATEGECTECACCACEAAGAATATECEGAACA 400
GRVER51.SEQ AGGTCTTGGAAGTCCAGTCTCGTACTAACTTCATCAAACG 440
         AGGTCTTGGAAGTCCAGTCTCGTACTAACTTCATCAAACG 440
GR6.SEQ
        AGGT CTTGGA A A GTCCA GTCTC GTACTA A CTTCATCAAACG 440
GRVER5.SEQ
GRVER4.SEQ AGGT CTTGGA AGTCCAGTCTCGTACTAACTTCATCAAACG 440
         AGGT CTTGGA AGT CCAGT CT CGT ACTAATTT CAT CAAACG 440
GRVER3.SEO
         AGGT|C|TTGGA|A|GT|G|CAG|TCTC|G|T|ACTAA|C|TTCAT|C|AA|GC|G 440
GRVER2.SEO
         AAGTCTTGGAAGTGCAGTCTCGTACTAACTTCATCAAGCG 440
GRVER1.SEO
YG81-6G1.SEQAGGTATTGGAGGTACAGAGCAGAACTAATTTCATAAAAG 440
RDVER1.SEQ AGGTGCTGGAGGTCCAAAGCCGCACCAATTTTATTAAACG 440
RDVER2.SEQ AAGTGCTTGGAGGTCCAAAGCCCGCACCAATTTTATTAAACG 440
RDVER3. SEQ A A G T G C T G G A A G T C C A A A G C C G C A A C T T T A T T A A G C G 440
RDVER4.SEQ AAAGTCCTTGGAAAGTCCAAAAGCCCGCAACTTTATTATTAAGCGG440
         AAGTCCTGGAAGTCCAAAGCCCGCACCAACTTTATTAAGCG
RDVER5.SEQ
         AAGTCCTGGAAGTCCAAAGCCCGCACCAACTTTATTAAGCG 440
RD7.SEO
RDVER51.SEQ AAGTIC CIT G G AAGTICIC AAA G CICIGICIA CICIA AICIT TITA TITA AG CIG 440
RDVER52.SEQ A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G 440
RD1561H9.SEQAAGTCCTGGAAGTCCAAAGCCGCACCAACTTTATTAAGCG 440
GRVER51. SEQ CATCATTATTCTGGATACCGTCGAAAACATCCACGGCTGT 480
         CATCAT TATTCTGGATACCGTCGAAAACATCCACGGCTGT 480
GR6.SEQ
         CATCATTATTCTGGATACCGTCGAAAACATCCACGGCTGT 480
GRVER5.SEO
         CATCATTATTCTGGATACCGTCGAAAACATCCATGGCTGT 480
GRVER4.SEQ
         CATTATTATTCTGGATACCGTCGAAAACATCCACGGCTGT 480
GRVER3.SEQ
         CATTATCATTCTGGATACCGTCGAGAATATCCACGGCTGT 480
GRVER2.SEQ
         CATTATCATTCTGGATACCGTCGAGAATATCCACGGCTGT 480
GRVER1.SEO
YG81-6G1.SEQG A T C A T C A T A C T T G A T A C T G T A G A A A C A T A C A C G G T T G T 480
         TATCATTATCTTGGACACTGTGGAAAACATTCATGGTTGC 480
RDVER1.SEO
         TATCATTATCTTGGACACTGTGGAAAACATTCATGGTTGC 480
RDVER2.SEO
         TATCATCATCTTGGACACTGTGGAGAATATTCATGGTTGC 480
RDVER3.SEO
         TATCATCATCTTGGACACTGTGGAGAATATTCACGGTTGC 480
RDVER4.SEQ
         TATCATCATCATCTTGGACACTGTGGAGAATATTCACGGTTGC 480
RDVER5.SEO
         TATCATCATICTTGG ACACTGTGG AGAATATTCACGGTTGC 480
RD7.SEQ
RDVER51.SEQ TATCATCATCTTGGACACTGTGGAGAATATTCACGGTTGC480
RDVER52.SEQ TATCATCTTGGACACTGTGGAGAATATTCACGGTTGC480
RD1561H9.SEQTATCATCTTGGACACTGTGGAGAATATTCACGGTTGC 480
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FIG. 2 (cont'd)

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GRUERSI. SEQ GAGAGCCT TOCCT A ACT T CATCT CT CGTTA CAGCGAT GGTA 520
          GAGAGCCTCCCTAACTTCATCTCTCGTTACAGCGATGGTA 520
GR6.SEQ
GRVER5.SEQ GAGAGCTCCCTAACTTCATCTCGTTACAGCGATGGTA 520
GRVER4.SEQ GAGAGCCTGCCTAACTTCATCTCTCGTTACAGCGATGGTA 520
GRVER3.SEQ GAGAGCTTGCCTAACTTTATCTCTCGTTACAGCGATGGTA 520
GRVER2.SEQ GAGAGCTTGCCAAAACTTTATTCTCGTTATAGCGACGGGTA 520
GRVER1.SEQ GAAAGCTTGCCAAAACTTTATTCTCGTTATAGCGACGGTA 520
YG81-6G1.SEQGAAAGTCTTCCCAATTTTATTTCTCGGTTATTCGGATGGAA 520
RDVER1.SEQ GAGTCTCTGCCTAATTTCATCAGCCGCTACTCTGATGGCA 520
RDVER2.SEQ GAAT CT CT GC CT AAT TT CAT CAG CCGCT ACT CT GAT G GC A 520
RDVER3.SEQ GAATCITCTGCCTAATTTCATTAGCCGCTATTCTGACGGCA 520
RDVER4.SEQ GAAT CITTIGCCITAATTTATTAGCCGCTATTCAGACGGAA 520
ROVERS. SEQ GAAT CITTIGC CITAATTICATCT CTCGCTATTCAGACGGCA 520
RD7. SEQ GAAT CITTIGCCTAATTTCATCT CTCGCCTATTCAGACGGCA 520
RDVER51.SEQ G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520
RDVER52.SEQ G A A T C T T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520
RD1561H9.SEQGAA<u>TC|TTTG|CCTAATTTC|ATCTCGCTATTCA</u>GACGGCA 520
GRVERSLSEQ ATATCGCTAATTTCAAGCCCTTGCATTTGATCCAGTCGA 560
GR6.SEQ ATATCGCTAATTTCAAGCCCTTGCATTTTGATCCAGTCGA 560
GRVERS.SEQ ATATCGCTAATTTCAAGCCCTTGCATTTTGATCCAGTCGA 560
GRVER4.SEQ ATATCGCTAATTTCAAACCACTGCATTTTGATCCAGTCGA 560
GRVER3.SEQ ATATCGCTAATTTCAAGCCACTGCATTTTGATCCAGTCGA 560
GRVER2.SEO ATATCGCTAACTTCAAGCCTCTGCATTTTGATCCAGTGGA 560
GRVERI.SEO ATATCGCTAACTTCAAGCCTCTGCATTTTGATCCAGTGGA 560
YG81-6G1.SEQ A T A T T G C C A A C T T C A A A C C T T T A C A T T T C G A T C C T G T T G A 560
RDVER1.SEQ ACATTGCCAATTTTAAACCATTGCACTTCGACCCTGTCGA 560
RDVER2.SEQ ACATTGCCAATTTTAAACCATTGCACTTCGACCCTGTCGA 560
RDVER3.SEQ ACATCGCCAACTTTAAACCTTTGCATTCGACCCTGTGGA 560
RDVER4.SEO ACATCGCCAACTTTAAGCCTCTCCATTTCGACCCTGTGGA 560
RDVERS.SEO ACATCGCAAACTTTAAACCACTCCACTTCGACCCTGTGGA 560
          A CATCGCAAACTTTAAACCACTCCACTTCGACCCTGTGGA 560
RD7.SEO
RDVER51.SEQ A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
RDVER52.SEQ A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
RD1561H9.SEQ A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
GRVER51.SEQ G C A A G T G G C C G C T A T T T T G T G C T C C C G G C A C C A C T G G T 600
       G C A A G T G G C C G C T A T T T T G T G C T C C T C C G G C A C C A C T G G T
GRVER5.SEQ GCAAGTGGCCGCTATTTTGTGCTCCTCCGGGCACCACTGGT 600
GRVER2.SEQ GCAAGT CGCCGCTATTTTTGTGCTCTAGCGGCACCACCGGT 600
GRVER1.SEQ GCAAGTCGCCGCTATTTTGTGCTCTAGCGGCACTACCGGT 600
YG81-6G1. SEQG CAAGTGGCAGCTATCTTATGTTCGTCAGGCACTACTGGA 600
RDVER1.SEQ - ACAGGTGGCTGCCATCCTGTGTAGCTCTGGTACCACTGGC
         ACAGGTGGCTGCCATCCTGTGTAGCTCTGGTACTACTGGC 600
RDVER2.SEO
RDVER3.SEQ A C A A G T G G C T G C T A T C C T G T G T A G C A G C G G T A C T A C T G G C 600
RDVER4.SEQ A CAAGTTGCTGCAATCCTGTGTGTAGCAGCGGTACTACTGGA 600
RDVER5.SEQ
         ACAAGTITGCAGCCATTCTGTGTGTAGCAGCGGTACTACTGGA 600
          A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
RD7.SEQ
RDVER51.SEO ALCAAGTITIG CAGCICIATIT CITIGIT GITLAGCAGCIGGITLACTACT GGA 600
RDVER52.SEQ A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
RD1561H9.SEQACAAGTTGCAGCCATTCTGTGTGTAGCAGCGGTACTACTGGA 600
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FIG. 2 (cont'd)

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GRVER51.SEQ TTGCCTAAAGGTGTCATGCAGACTCACCAGAATATCTGTGTG
         TTGCCTAAAGGTGTCATGCAGACTCACCAGAATATCTGTG 640
GR6.SEO
GRVER5.SEQ TT GCCT AAAGGTGT CATGCA GACTCACCA GAATAT CTGTG 640
GRVER4. SEQ TT G C C T A A A G G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G 640
GRVER3.SEQ TTGCCTAAAGGTGTCATGCAGACTCACCAGAATATCTGTG 640
        CTCCTAAAGGCGTGATGCAGACTCACCAAAATATCTGTG 640
GRVER2.SEQ
GRVER1.SEQ CTGCCTAAAGGCGTGATGCAGACTCACCAAAATATCTGTG 640
YG81-6G1.SEQTTACCGAAAGGTGTAATGCAAACTCACCAAAATATTTGTG 640
RDVER1.SEQ TTGCCAAAGGGTGTCATGCAAACCCATCAGAACATTTGCG 640
        TTGCCAAAGGGTGTCATGCAAACCCATCAGAACATTTGCG 640
RDVER2.SEQ
        CTCCCAAAGGGCCGTCATGCAGACCCATCAAAACATTTGCG 640
RDVER3.SEQ
        CTCCCAAAGGGAAGTCATGCAGACCCATCAAAACATTTGCG 640
RDVER4.SEQ
        CITICIC CIAIA AIGIG GIAIG TICIA T G C AIGIA CICIC AITIC A A A AICIA T T T GICIG 640
RDVER5.SEQ
        CTCCCAAAGGGGAGTCATGCAGACCCATCAAAACATTTGCG 640
RD7.SEO
RDVER51. SEQ CTCCAAAAGGGGAGTCATGCAGACCCATCAAAACATTTGCG 640
RDVER52.SEQ CTCCCAAAAGG GAGTCATGCAGACCCATCAAAACATTTGCG 640
RD1561H9.SEQCTCCCAAAGGGAGTCATGCAGACCCATCAAAACATTTGCG 640
GRVER51.SEO TGC GT TTGATCC ACGC TCTCG ACCCTT GTGT GG GTACTC A 680
         TIGIC GIT TITIGIA TICIC AICIG C TICITICIG A C C CIT C GITIGIT G G G TIA CITIC A 680
GRVERS.SEQ TIGIC GIT TITIGIA TICIC AICIG C TICITICIG A C C CIT CIGITIGIT GIG GIT A CITIC A 680
GRVER4.SEQ T GC GT TTGATCC ACG TTCTCGACCCTCGTGTGT GGGTACTCA 680
GRVER3.SEQ TGCGCTTGATCCACGCCTTCGACCCTTCGTGTGGGGTACTCA 680
GRVER2.SEQ TCCGCTTGATTCATGCCCTTGGACCCACGTGTGTGGGGTACTCA 680
GRVERI.SEQ TCCGCTTGATTCATGCCCTGGACCCACGTGTGGGTACCCA 680
YG81-6G1.SEQ T C C G A C T T A T A C A T G C T T T A G A C C C C A G G G C A G G A A C G C A 680
RDVERLSEQ TGC GTC TGA TCC ACGC TCTCG ATC CT CGC TACGGCA CTCA 680
RDVER2.SEQ TIGIC GITIC TIGIA TICIC ACIG C TICITICIG ALTIC CIT CIGIC T A CIG GICIA CICIC A 680
RDVER3.SEQ TIGIC GITIC TIGIA TICIC AT G C TICITICIG AITIC CIA CIGIC TA CIG GICIA CITIC A 680
RDVER4.SEQ TIGIC GITIC TIGIA TICIC A T G C TICITICIG A TIC CIA CIGIC T A CIG GICIA CITIC A 680
RDVERS.SEQ T GCGTCTGATCCATGCTCTGATCCACGCTACGGCACTCA 680
RDZ.SEQ T GCGTCTGATCCATGCTCTGGATCCACGCTACGGCACTCA 680
RDVER51.SEQ T GC GTC T GATCCATGCT CTC ATCCACGC ACGCTACGGCACTCA 680
RDVER52.SEQ TGC GTC TGATCCATGCTCTCGATCCACGCTACGGCACTCA 680
RD1561H9.SEQ TGCGTCTGATCCATGCTCTCGATCCACGCTACGGCACTCA 680
GRVER51.SEQ ATTGATCCCTGGCGTGACTGTGCTGGTGTATCTGCCTTTC 720
         ATTGATCTCTGGCGTGACTGTGCTGGTGTATCTGCCTTTC 720
GR6.SEQ
GRVERS.SEO A T T GAT C CTGGC TGGC TGACT GTGCT GTGT ATCTGCCTTTC 720
 GRVER4. SEQ ATTGATCCCTGGCGTGACTGTGCTGGTGTATCTGCCTTTC 720
 GRVER3.SEQ ATTGATCCCTGGCGTGACTGTCTGCTGTATTTGCCTTTTC720
 GRVER2.SEQ GTTGATCCCTGGCGTGACTGTCCTGGTGTACTTGCCATTCC720
         GTTGATCCCTGGCGTGACTGTCCTGGTGTACTTGCCATTC 720
 GRVER1.SEQ
 YG81-6G1. SEQACTTATTCCTGGTGTGACAGTCTTAGTATATCTGCCTTTT 720
 RDVER1. SEQ ACTGATTCCAGGTGTCACCGTGTTGGTCTATCTGCCTTTT 720
 RDVER2.SEQ ACT GATTCTTGTTCACCTGTTTT 720
 RDVER3.SEQ GCTGATTCCTGGTGTCACCGTCTTGGTCTACCTGCCTTTC 720
 RDVER4.SEQ GCTGATTCCTGGTGTCACCGTCTTGGTCTACTTTGCTTTGCCTTTC 720
         GCTGATTCCTGGTGTCACCGTCTTGGTCTACTTGCCTTTC 720
 RDVER5.SEO
         GCTGATTCCTGGTGTCACCGTCTTGGTCTTACTTGCCTTTC 720
 RD7.SEO
 RDVER51. SEQ GCTGATTCCTGGTGTCACCGTCTTGGTCTACTTGCTACTTC 720
 RD1561H9.SEQGCTGATTCCTGGTGTCACCGTCTTGGTCTACTTGCCTTTC 720
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FIG. 2 (cont'd)

```
GRVER51. SEQ TTTCACGCCTTTGGTTTCTCTATTACCCTTGGCTATTTCA 760
         TTTCACGCCTTTGGTTTCTCTATTACCCTGGGCTATTTCA 760
GR6.SEO
GRVER5.SEQ TTTCACGCTTTGGTTTCTCTATTACCCTGGGCTATTTCA 760
GRVER4.SEQ TITICA CIGCICITTTGG|T|TTTTTTTAT|T|ACC|C|TGGG|C|TA|T|TTCA 760
GRVER3.SEQ TTTCACGCCTTTTGGTTTTTTTTTTTTTCACCCTTGGGCCTATTTTCA 760
GRVER2.SEQ TTTCACGCCTTCGGGTTTTTTCTATTACCCTGGGCTATTTCA 760
GRVER1.SEQ TTTCACGCCTTCGGTTTTTCTATTACCCTGGGCTATTTCA 760
YG81-6G1.SEQTTCCATGCTTTTGGGTTCTCTATAACCTTGGGATACTTCA 760
RDVER1.SEQ TTCCATGCTTTTGGCTTCCACATCACTTTGGGTTACTTTA 760
RDVER2.SEQ TTCCATGCTTTTGGCTTTCCACATCACTTTGGGTTACTTTA 760
RDVER3.SEQ TTCCATGCTTTCGGCTTCCACATTACTTTGGGTTACTTTA 760
RDVER4.SEQ TTCCATGCTTTCGGCTTTCCATATTACTTTGGGTTACTTTA 760
RDVER5.SEQ TTCCATGCTTTCGGCTTTCATATTACTTTGGGTTACTTTA 760
         TTCCATGCTTTCGGCTTTCATATTACTTTGGGTTACTTTA 760
RD7.SEO
RDVER52.SEQ TTCCATGCTTTCGGGCTTTCATTATTACTTTGGGTTACTTTA 760
RD1561H9.SEQT T C C A T G C T T T C G G C T T T C A T A T T A C T T T G G G T T A C T T T A 760
GRVER51.SEO TGGTCGGCTTGCGTGTCATCATGTTTCGTCGCTTCGACCA 800
GR6.SEO
         TGGTCGGCTTGCGTGTCATCATGTTTCGTCGCTTCGACCA 800
GRVERS.SEO TEGTICIGECTTEGCGTGTCATCATGTTTCGTCGTCGICTTCGACCA 800
GRVER4.SEO TGGTCGGCTTGCGTGTCATCATGTTTCGTCGCTTCGACCA 800
GRVER3.SEO TEGTICEGICTITECGTGTEATCATETTTCETCGTCGCTTCEGAICCA 800
GRVER2.SEO TGGTCGGTTTTGCGCGCGTGATCATGTTTCGTCGCTTCGATCA 800
GRVER1.SEQ TGGTCGGTTTGCGCGTGATCATGTTTCGTCGCTTCGATCA 800
YG81-6G1.SEO T G G T G G T C T T C G T G T T A T C A T G T T C A G A C G A T T T G A T C A 800
RDVER1.SEQ TGGTGGGCCTGCGTGTCATTATGTTCCGCCGTTTTTGACCA 800
RDVER2.SEO TGGTGGGCCTGCGTGTCATTATGTTCCGCCCGTTTTTGACCA 800
RDVER3.SEO TGGTCGGTCTGCGTGTCATTATGTTCCGCCGTTTTTGATCA 800
RDVER4.SEQ TGGTCGGTCTGCGTGTGATTATGTTCCGGCCGTTTTGATCA 800
RDVERS.SEO TGGTCGGTCTCCGCGTGATHATGTTCCGGCCGHTTTTGATCA 800
         TGGTCGGTCTCCGCGTGATTATGTTCCCCCCCTTTTTGATCA 800
RD7.SEO
RDVER51.SEO T G G T C G G T C T C C G C G T G A T T A T G T T C C G C C G T T T T G A T C A 800
RDVER52.SEO TGGTCGGTCTCCGCGCGTGATTATGTTCCCGCCGTTTTTGATCA 800
RD1561H9.SEQTGGTC|GGTCT|CGGCGTGAT|TATGTTC|CGCCGTTTTTGATCA 800
GRVER51.SEQ AGAAGCCTTCTTGAAGGCTATTCAAGACTACGAGGTGCGT
GR6.SEO
         AGAAGCCTTCTTGAAGGCTATTCAAGACTACGAGGTGCGT 840
GRVER5.SEQ AGAAGCICITIC TITIGAAGGCTATTCAAGAICITAICGAIGGTIGICGII 840
GRVER4. SEQ AGAAG CICITTIC TITIGIAA GIG CTATTCA ALGAICITAICIGA GIG TIGIC GITI 840
GRVER3. SEQ AGAAGCCTTCCTGAAGGCTATTCAAGGACTACGAGGTGCGT 840
GRVER2.SEQ AGAAGC|C|TTTCT|G|A|G|GC|C|ATTCA|A|GA|C|TA|C|GA|G|GT|C|CG|T|840
GRVER1.SEQ AGAAGCTTTTCTGAAGGCCATTCAGGACTACGAGGTCCGT 840
YG81-6G1.SEQAGAAGCATTTCTAAAAGCTATTCAGGATTATGAAGTTCGA 840
RDVER1. SEQ. GGAGG CCTTCTTGAAAGCTATCCAAGATTATGAAGTGCGC 840
RDVER2.SEO
        GGAGGCTTTCTTGAAAGCTATCCAAGATTATGAAGTGCGC 840
RDVER3.SEQ
        GGAGGCTTTTTTGAAAGCCATCCAAGATTATGAAGTCCGC 840
        GGAGGCTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGC 840
RDVER4.SEQ
RDVER5.SEQ
        GG AGG CTTTCTTGAAAGCCATCCAAAGATTATGAAGTCCGC 840
         GGAGGCTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGC 840
RD7.SEO
RDVER51. SEQ GG A GG C T T T C T T GA A A G C C A T C C A A G A T T A T G A A G T C C G C 840
RDVER52. SEQ GG G A G G C T T T C T T T G A A G C C A T C C A A G A T T A T G A A G T C C G C 840
RD1561H9.SEQGGAGGCTTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGC 840
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FIG. 2 (cont'd)

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TCCGTGATCAACGTCCCTTCAGTCATTTTGTTCCTGAGCA 880
 GRVER5.SEO
 GRVER4.SEO
         TCTGTCATCAATGTCCCTTCAGTCATTTTGTTCCTGAGCA 880
         TCT GTGATCAATGTCCCATCTGTCATTTTGTTCCTGAGCA 880
 GRVER3.SEQ
          AGCGTGATCAACGTCCCTTCTGTGATTTTTGTTCCTGAGCA 880
 GRVER2.SEO
 GRVER1.SEO
          AGICIG TIGIATICIA ACGTICIC CITIT CITIG TIGIATITT TGTT CICITIG AGCIA 880
 YG81-6G1. SEQAGTGTAATTAACGTTCCATCAGTAATATTGTTCTTATCGA 880
          TCTGTCATTAATGTGCCAAGCGTCATCCTGTTTTTGTCTA 880
 RDVER1.SEO
         T CT GT CATTAATGTGC CAAGCGTCATCCTTGTTTTTGTCTA 880
 RDVER2.SEQ
 RDVER3. SEQ A GC G T C A T T A A C G T G C C T A G C G T G A T C C T G T T T T T T G T C T A 880
 RDVER4.SEQ AGTGT CATCAACGT GCCT AGCGT GATCCT GTTTTT GTCTA 880
 RDVER5.SEQ AGTGTCATCAACGTGCCTAGCGTGATCCTGTTTTTTTTTA 880
          AGTGTCATCAACGTGCCTAGCGTGATCCTGTTTTTTGTCTA 880
 RDVER52.SEQ AGTGT|C|AT|C|AACGT|G|CC|TAGC|GT|G|AT|CC|TGTT|TTT|G|TC|T|A 880
 RD1561H9.SEQAGTGTCATCAACGTGCCTAGCGTGATCCTGTTTTTGTCTA 880
GRVER51.SEQ AAT CITCCTTTGGTTGACAAGTATGATCTGAGCAGCTTGCG 920
GR6.SEO
          AATCTCCTTTGGTTGACAAGTATGATCTGAGCAGCTTGCG 920
GRVER5.SEQ AAIT CIT C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G 920
GRVER4.SEQ AATCITCCTTTGGTTGACAAGTATGATCTGAGCAGCTTGCG 920
GRVER3.SEQ AAIT CITCCTTTGGTTGACAAGTAIGATCITGAGCIAGCITTGCG 920
GRVER2.SEQ AAT CIT C CATT G G T C G A T A A G T A T G A C C T G A G C A G C T T G C G 920
GRVERI.SEQ A ATCTCCATTGGTCGATAAGTATGACCTGAGCTCTTTGCG 920
YG81-6G1.SEQ AAAGT C C T T T G G T T G A C A A T A C G A T T T A T C A A G T T T A A G 920
RDVER1.SEQ AGAGCCCTCTGGTGGACAAATACGATTTGTCTAGCCTGCG 920
RDVER2.SEQ AGAGCCCTCTGGTGGACAAATACGATTTGTCTTCTGCG 920
RDVER3.SEQ AGAGCCCACITCGTGGACAAGTACGACTTGTCTTCCCTGCG 920
RDVER4.SEQ A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T C A C T G C G 920
RDVER5.SEQ AGAGCCCACTCGTGGACAAGTACGACTTGTCTTCACTGCG 920
RD7.SEO
          A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G 920
RDVER51.SEQ AGA GCCCACTCGTGGACAAGTACGACTTGTCACTGCG
RDVER52.SEQ AGA GCCCACTCGTGGACAAGTACGACTTGTCTTCACTGCG 920
RD1561H9.SEQ AGA GCCCA CTCG TGG A C A AGT A C G ACT TGT CTT C A CTG CG 920
GRVER51.SEO ITIG AG CIT GIT GET GET GET GET CTT TGG CCA A A G A G TG 960
          TIG AIG CIT G T GICIT GITIG GICIG CITIG CITIT TIGIG CICIA A A G A G TIGI
GR6.SEO
GRVER5.SEO
          TIGAG CIT GT GICIT GITIG GICIG CITIC CITIT TIGIG CICIA A A GA A GT GI
         ITIG AIG CIT G T GICIT GITIG GICIG CITIG CITIT TIGIG CICIA A A G A A G TIGI 960
 GRVER4.SEO
         TIGAACT GT GCT GTG GCG CTG CTC CTTT TGG CCAAAGAA GTG 960
 GRVER3.SEO
         CGAACTGTGCTGTGGCGCTGCCCTTTTGGCTAAAGAGGTG
 GRVER2.SEO
 GRVERL. SEQ CGAACT GTGCTGTGCCCCTTTTGGCTAAAGAGGTG 960
 YG81-6G1. SEOG G A A T T G T G T T G C G G T G C G G C A C C A T T A G C A A A G A A G T T 960
          TIGAGT T G T G T T G C G G T G C C G C T C C A C T G G C C A A G G A A G T C 960
 RDVER1.SEO
          TIGAGITT GTGTTGCGGTGCCGCTCCACTGGCCAAGGAAGTC 960
 RDVER2.SEO
         TGAGTTGTGTTGCGGTGCCGCCCCACTGGCTAAGGAGGTC 960
 RDVER3.SEO
         TIGAATTGTGTTGCGGTGCCGCTCCACTGGCTAAGGAGGTC 960
 RDVER4.SEO
 RDVER5.SEO
          TGAATTGTGTTGCGGTGCCGCTCCACTGGCTAAGGAGGTC 960
          TIGAATTGTGTTGCGGTGCCGCTCCACTGGCTAAGGAGGTC 960
 RD7.SEO
 RDVER51.SEO TIG A A T T G T G T T G C G G T G C C G C T C C A C T I G G C T A A G G A G G T C C 960
 RDVER52. SEQ TIGAATTGTGTTGCGGTGCCGCTCCACTGGCTAAGGAGGTC 960
 RD1561H9. SEQTIG A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C 960
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FIG. 2 (cont'd)

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GRVER51.SEQ G C C G A G G T C G C T G C T A A G C G T C T G A A C C T C C T G G T A T C C 1000
           G C C G A G G T C G C T G C T A A G C G T C T G A A C C T C C C T G G T A T C C 1000
 GR6.SEO
           G C C G A G G T C G C T G C T A A G C G T C T G A A C C T C C C T G G T A T C C 1000
 GRVER5.SEO
 GRVER4.SEQ G C C G A G G T C G C T A A G C G T C T G A A C C T C C C T G G T A T C C 1000
 GRVER3.SEQ G C C G A G G T C G C T G C T A A G C G T C T G A A C C T C C T G G T A T C C 1000
 GRVER2. SEO GCCG AAG TCG CCTG CCCA AGC GT CTGA ATT T GC CA G GTA TCC 1000
 GRYERI. SEQ G C G A A G T T G C C A A G C G T C T G A A T T T G C C A G G T A T C C 1000
YG81-6G1. SEQ G C T G A G G T T G C A G C A A A A C G A T T A A A C T T G C C A G G A T T C 1000
 RDVER1.SEQ GCTGAGGTGGCCGCTAAACGCTTGAACCTGCCTGGCATTC 1000
 RDVER2.SEQ GCTGAGGTGGCCGCTAAACGCTTGAACCTTGCCTTGGCATTC 1000
 RDVER3.SEQ GCTGAAGTGGCCGCCAAACGCTTGAATCTGCCAGGCATTC 1000
 RDVER4.SEQ GCTGAIAGTIGGCCGCCAAACGCTTGAATCTGCCCGGCATTC 1000
 RDVER5.SEQ GCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC 1000
           GCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC 1000
 RD7.SEQ
 RDVER51.SEQ G C T G A A G G G C C G C C A A A C G C T T G A A T C T T C C A G G G A T T C 1000
 RDVER52.SEQ G C T G A A G G C C G C C A A A C G C T T G A A T C T T C C A G G G A T T C 1000
 RD1561H9.SEQGCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC 1000
GRVER51.SEQ G C T G C G G T T T T G G T T T G A C T G A G A G C A C T T C T G C T A A C A T 1040
GR6.SEO
           GCTGCGGTTTTGGTTTGACTGAGAGCACTTCTGCTAACAT 1040
GRVER5.SEQ GCTGCGGTTTTGGTTTGACTGAGAGCACTTCTGCTAACAT 1040
GRVER4.SEQ GCTGCGGTTTTGGTTTGACTGAGAGCACTTCTGCTAACAT 1040
GRVER3.SEQ GCTGCGGTTTTGGTTTGACTGAGAGCACTTCTGCCAACAT 1040
GRVER2.SEQ GCTGCGGCTTTGGTCTGACTGAGAGCCACCTCTGCTAACAT 1040
GRVERI.SEQ GCTGCGGCTTTGGTCTGACTGAGAGCCCCTCTGCTAACAT 1040
YG81-6G1.SEO G C T G T G G A T T T G G T T T G A C A G A A T C T A C T T C A G C T A A T A T 1040
RDVER1.SEQ GTTGTGGTTTCGGCTTGACCGAATCTACTAGCGCCATTAT 1040
RDVER2.SEQ GTTGTGGGTTTTCGGCCTTGACCGAATCTACTAGCGCCATTAT 1040
RDVER3.SEQ GITGTGGCTTCGGCCTTCACCGAATCTACCAGCGCTAITAT 1040
RDVER4.SEQ GITTGTGGCTTCGGCCTTCACCGAATCTACCAGCGCTATTAT 1040
RDVER5.SEQ GITTGTGGCTTCGGCCTCACCGAATCTACCAGCGCTAITAT 1040
RD7.SEO
           GITIT G T G GICIT TICIG GIC CITICIA CICIG A A T C T A CIC A G CIG C T AITIT A T 1040
RDVER51.SEQ GITTGTGGCTTCGGCCTCACCGAATCTACCAGCGCTAITAT 1040
RDVER52.SEQ GTTGTGGCTTCGGCCTCACCGAATCTACCAGCGCTATTAT 1040
RD1561H9.SEQGTTGTGGCTTCGGCCTCCACCGAATCTACCAGTGCGATTAT 1040
GRVER51.SEQ CCATAGCTTGCGAGACGAGTTTAAGTCTGGGTAGCCTGGGT1080
GR6.SEQ CCATAGCTTGCGAGACGAGTTTAAGTCTTGGTAGCCTGGGT1080
           CCATAGCTTGCGAGACGAGTTTAAGTCTGGTAGCCTGGGT 1080
GRVER5.SEO
           CCATAGCTTGCGAGACGAGTTTAAGTCTGGTAGCCTGGGT 1080
 GRVER4.SEQ
           CCATAGCTTGCGTGACGAGTTTAAATCTGGTAGCCTGGGT 1080
 GRVER3.SEQ
 GRVER2.SEQ
           TICATAGCTTGCGTGATGAGTTCAAATCTGGCAGCCTGGGT 1080
           TCATAGCTTGCGTGATGAATTCAAATCTGGCAGCCTGGGT 1080
 YG81-6G1. SEQACACAGTCTTAGGGATGAATTTAAATCAGGATCACTTGGA 1080
           CCAATCTCTGCGCGACGAGTTTAAGAGCGGTTCTTTGGGC 1080
 RDVER1.SEQ
           CCAATCTCTGCGCGACGAATTTAAGAGCGGTTCTTTGGGGC 1080
 RDVER2.SEQ
 RDVER3.SEQ
           ITIC ALAT CIT C TIC CIGICIG A T G AGIT T T A AIG A G CIG GICIT CIT TITIGIG GIC 1080
           T C A G T C T C T C C G C G A T G A G T T T A A G A G C G G C T C T T T G G G C 1080
 RDVER4.SEQ
           TICAGT CITCTIC CIGICIG AT GAIGITT TAAIGAG CIGGICIT CITTITIGIG GICI 1080
 RDVER5.SEQ
           ITIC AIG T CIT C TIC CIGICIG A T G AIGIT T T A AIG A G CIG GICIT CIT TITIGIG GICI 1080
 RDVER51. SEQ TIC A G T CT C T C C G C G A T G A G T T T A A G A G C G G C T C T T T G G G C 1080
 RDVER52. SEQ TICAGTCTCTCGGGGATGAGTTTAAGAGAGCGGCTCTTTGGGGC 1080
 RD1561H9. SEQC CAGACT CT CGGGGATGAGTTTAAGAGCGGCTCTTTGGGGC 1080
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FIG. 2 (cont'd)

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CGCGTGACTCTTATGGCTGCAAAGATCGCCGACCGTG 1120
CGCGGTGACTCTCTTATGGCTGCAAAGATCGCCGAACCGTG 1120
CGCGTGACTCTTTATGGCTGCAAAGATCGCCGAACCGTG 1120
 GRVER51.SEQ
 GR6.SEQ
 GRVER5.SEQ
 GRVER4.SEQ
            CGTGACTCCTCTTATGGCTGCAAAGATCGCCGACCGTG 1120
            CGTGACCCCTTTGATGGCTGCAAAGATCGCCGACCGTG 1120
 GRVER3.SEQ
            CGTGACTCCTTTGATGGCCGCTAAGATCGCCGACCGTG 1120
 GRVER2.SEQ
          CGCGTGACTCCTTTGATGGCCGCTAAGATCGCCGACCGTG 1120
 GRVER1.SEO
 YG81-6G1. SEQAGAGTTACTCCTTTAATGGCAGCTAAAATAGCAGATAGGG 1120
         CGTGTCACCCCACTGATGGCTGCCAAAATTGCTGATCGCG 1120
 RDVER1.SEQ
          CGTGTCACCCCACTGATGGCTGCCAAAATTGCTGATCGCG 1120
 RDVER2.SEQ
          CGTGTCACTCCACTCATGGCTGCTAAAATCGCTGATCGCG 1120
 RDVER3.SEQ
          CGTGTCACTCCACTCATGGCTGCTAAGATCGCTGATCGCG 1120
 RDVER4.SEQ
          CGTGTCACTCCACTCATGGCTGCTAAGATCGCTGATCGCG
 RDVER5.SEQ
 RD7.SEQ
          CGTGTCACTCCACTCATGGCTGCTAAGATCGCTGATCGCG 1120
 RDVER51. SEQ CGTGTCACTCCACTCATGCTGCTAAGATCGCTGATCGCG120
 RDVER52. SEQ CGTGTCACTCCACTCGATGGCTGCTAAGATCGCTGATCGCGGGG 1120
 RD1561H9.SEQCGTGTCACTCATGGCTGCTAAGATCGCTGATCGCG 1120
GRVER51.SEQ AGA CCG GCA A A G C ACT G G GCC C A A A T C A A G T CG G T G A A T T 1160
          AGACCGGCAAAGCACTGGGCCCAAATCAAGTCGGTGAATT 1160
GR6.SEO
GRVER5.SEO
          AGACCGGCAAAGCACTGGGCCCAAATCAAGTCGGTGAATT 1160
GRVER4.SEQ AGACCGGCAAAGCACTGGGCCCAAATCAAGTCGGTGAATT 1160
GRVER3.SEQ AGACCGGCAAAGCCCTGGGCCCAAATCAGGTCGGTGAATT 1160
GRVER2.SEQ AGACCGGCAAAGCTCTGGGTCCAAATCAAGTCGGCGAATT 1160
GRVER1.SEQ AGACCGGCAAAGCTCTGGGTCCAAATCAAGTCGGCGAATT 1160
YG81-6G1.SEQ AAACTGGTAAAGCATTGGGACCAAATCAAGTTGGTGAATT 1160
RDVER1.SEQ AAACTGGTAAGGCCTTGGGCCCTAACCAGGTGGGTGAGCT 1160
RDVER2.SEQ AAACTGGTAAGGCCTTGGGCCCTAACCAGGTGGGTGAGCT 1160
RDVER3.SEO AAACTGGTAAGGCTTTTGGGCCCTAACCAAGTGGGCCGAGCT 1160
RDVER4.SEQ AAACTGGTAAGGCTTTTGGGCCCTAACCAAGTGGGGCGAGCT 1160
RDVERSSEQ AAACTGGTAAGGCTTTTGGGCCCTAACCAAGTGGGCGAGCT 1160
RD7.SEQ AAACTGGTAAGGCTTTTGGGCCCGAACCAAGTGGGCGAGCT 1160
RDVER51.SEO A A A C T G G T A A G G C T T T G G G C C G A A C C A A G T G G G C G A G C T 1160
RDVER52.SEO A A A C T G G T A A G G C T T T G G G C C C G A A C T G G G G G G A G C T 1160
RD1561H9.SEO A A A C T G G T A A G G C T T T G G G C C G A A C C A A G T G G G G A G C T 1160
GRVER51.SEQ GT GT ATTAAGG GCC CTATGGTCT CTAAAGGCTACGTGAAC 1200
GR6.SEO
          GTGTATTAAGGGGCCTATGGTCTCTAAAGGCTACGTGAAC 1200
GRVER5.SEO
          GTGTATTAAGGGCCCTATGGTCTCTAAAGGCTACGTGAAC 1200
          GTGTATTAAGGGGCCCTATGGTCTCTAAAGGCTACGTGAAC 1200
 GRVER4.SEQ
 GRVER3.SEO
          GTGCATTAAGGGGCCCTATGGTCTCTAAAGGCTACGTGAAC 1200
          GTGTATTAAGGGTCCTATGGTGTCTAAAGGCTACGTCAAC 1200
 GRVER2.SEO
          GTGTATTAAGGGTCCTATGGTGTCTAAAGGCTACGTCAAC 1200
 GRVER1.SEO
 YG81-6G1. SEQATGCATTAAAGGTCCCATGGTATCGAAAGGTTACGTGAAC 1200
          GTGCATCAAAGGCCCAATGGTCAGCAAGGGTTATGTGAAT 1200
 RDVER1.SEO
 RDVER2.SEO
          GTGCATCAAAGGCCCAATGGTCAGCAAGGGTTATGTGAAT 1200
          GTGTATCAAAGGCCCTATGGTGAGCAAGGGTTATGTCAAT 1200
 RDVER3.SEO
          GTGTATCAAAGGCCCTATGGTGAGCAAGGGTTATGTCAAT 1200
 RDVER4.SEO
 RDVER5.SEQ
          GTGTATCAAAGGCCCTATGGTGAGCAAGGGTTATGTCAAT 1200
          GT GTATCAAA GGCCCTAT GGTGAGCAAGGGTTATGTCAAT 1200
 RD7.SEQ
          GTGTATCAAAGGCCCTATGGTGAGCAAGGGTTATGTCAAT 1200
 RDVER52. SEQ GIT GIT A T C A A A G G C C C T A T G G T G A G C A A G G G T T A T G T C A A T 1 200
 RD1561H9. SEC GT GT AT CAAAGGCCCTAT GT GT GAGCAAGGGTT AT GT CAAT 1200
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FIG. 2 (cont'd)

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GRVER51. SEQ A A T G T G G A G G C C A C T A A A G A A G C C A T T G A T G A T G G T G C T 1240
          AATGTGGAGGCCACTAAAGAAGCCATTGATGATGATGGCT 1240
AATGTGGAGGCCACTAAAGAAGCCATTGATGATGATGGCT 1240
 GR6.SEO
 GRUFRS SEO
 GRVER4.SEQ AATGTGGGAGGCCACTAAAGAAGCCATTGATGATGATGGCT 1240
 GRVER3. SEQ AATGTGGGAGGCCACTAAAGAAGCTATTGATGATGATGGTT 1240
          AATGTGGAGGCCACTAAGGAAGCTATTGATGACGATGGTT 1240
 GRVER2.SEQ
          AATGTGGAGGCCACTAAGGAAGCTATCGATGACGATGGTT 1240
 GRVER1.SEQ
 YG81-6G1. SEO A A T G T A G A A G C T A C C A A A G A A G C T A T T G A T G A T G A T G G T T 1240
 RDVER1. SEQ AACGTCGAAGCTACCAAAGAGGCCATTGACGATGACGGCT 1240
 RDVER2.SEQ AACGTCGAAGCTACCAAAGAGGCCCATCGACGATGACGGCT 1240
 RDVER3.SEO A A C G T C G A A G C T A C C A A G G A G G C C A T C G A C G A C G G C T 1240
 RDVER4.SEO A A C G T C G A A G C T A C C A A G G A G G C T A T C G A C G A C G A C G G C T 1240
 RDVER5. SEO A A C G T C G A A G C T A C C A A G G A G G C G A T C G A C G A C G G C T 1240
          A A C G T T G A A G C T A C C A A G G A G G C C A T C G A C G A C G G C T 1240
 RD7.SEO
 RDVER51.SEQ A A C G T T G A A G C T A C C A A G G G G C C A T C G A C G A C G G C T 1240
 RDVER52.SEQ A A C G T T G A A G C T A C C A A G G A G G C C A T C G A C G A C G G C T 1240
 RD1561H9.SEQA ACG TIGA AGCTACCA AGGAGGCCATCGACGACGACGGCT 1240
GRVER51.SEQ G G C T C C A T A G C G G C G A C T T C G G T T A C T A T G A T G A G G A C G A 1280
GR6.SEO
          GGCTCCATAGCGGCGACTTCGGTTACTATGATGAGGACGA 1280
GRVER5.SEQ GGCT|C|CA|TAGC|GG|C|GACTT|C|GG|TTACTATGATGAGGA|C|GA 1280
GRVER4.SEQ GGCTCCATAGCGGCGACTTCGGTTACTATGATGAGGACGA 1280
GRVER3.SEQ GGTTGCATAGCGGCGACTTCGGTTATTATGATGAGGACGA 1280
GRVER2.SEQ GGCTGCACAGCGGCGACTTTGGTTATTACGATGAGGACGA 1280
GRVER1.SEQ GGCTGCACAGCGGCGACTTTGGTTATTACGATGAGGACGA 1280
YG81-6G1.SEQ G G C T T C A C T C T G G A G A C T T T G G A T A C T A T G A T G A G G A T G A 1280
RDVER1.SEQ GGTTGCATTCTGGTGATTTCGGCCTACTATGACGAAGATGA 1280
RDVER2.SEQ GGTTGCATTCTGGTGATTTCGGGCTACTATGACGAAGATGA 1280
RDVER3.SEQ GGCTGCATTCTGGTGATTTTGGCTACTACGACGAAGATGA 1280
RDVER4.SEQ GGTTGCATTCTGGTGATTTTGGATATTACGACGAAGATGA 1280
G G T T G C A T T C T G G T G A T T T T G G A T A T T A C G A C G A A G A T G A 1280
RDVER51.SEQ G G T T G C A T T C T G G T G A T T T T G G A T A T T T A C G A C G A A G A T G A 1280
RDVER52.SEQ G G T T G C A T T C T G G T G A T T T T G G A T A T T T A C G A C G A A G A T G A 1280
RD1561H9.SEQ G G T T G C A T T C T G G T G A T T T T G G A T A T T A C G A C G A A G A T G A 1280
GRVER51.SEQ ACACTTCTATGTGGTCGATCGCTACAAAGAATTGATTAAG 1320
          A C A C T T C T A T G T G G T C G A T C G C T A C A A A G A A T T G A T T A A G 1320
          ACACTTCTATGTGGTCGATCGCTACAAAGAATTGATTAAG 1320
GRVER5.SEQ
          ACACTTCTATGTGGTCGATCGCTACAAAGAATTGATTAAG 1320
 GRVER4.SEO
          ACACTTCTATGTGGTCGATCGCTATAAAGAATTGATTAAG1320
 GRVER3.SEO
          ACATTTCTATGTCGTCGATCGCTACAAAGAGTTGATTAAG 1320
 GRVER2.SEO
          ACATTTCTATGTCGTGGATCGCTACAAAGAGTTGATTAAG 1320
 GRVER1.SEO
 YGB1-6G1.SEQG CATTTCTATGTGGTGGACCGTTACAAGGAATTGATTAAA 1320
 RDVER1.SEQ GCACTTTTACGTGGTCGACCGTTATAAGGAACTGATCAAA 1320
 RDVER2.SEQ GCACTTTTTACGTGGTGGACCGTTATAAGGAACTGATCAAA 1320
 RDVER3.SEQ GCATTTTTACGTCGTGGATCGTTACAAGGAGCTGATCAAA 1320
 RDVER4.SEQ GCATTTTTACGTCGTGGATCGTTACAAGGAGCTGATCAAA 1320
 RDVER5.SEQ GCATTTTTTACGTCGTGGATCGTTACAAGGAGCTGATCAAA 1320
          GCATTTTTACGTCGTGGATCGTTACAAGGAGCTGATCAAA 1320
 RDVER51.SEQ G C A T T T T T A C G T C G T G G A T C G T T A C A A G G A G C T G A T C A A A 1320
 RDVER52.SEQ GCATTTTTACGTCGTGGATCGTTACAAGGAGCTGATCAAA 1320
 RD1561H9.SEQGCATTTTTTACGTCGTGGATCGTTACAAGGAGCTGATCAAA 1320
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FIG. 2 (cont'd)

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GRVER51.SEQ TACAAAGGCTC TCAAGTCGCACCAGCCGAACTGGAAGAAA 1360
          TAICIA AIAIG G C T C T CAIAIG TICIG C A C CIAIG CICIG A A C TIGIG A A G AIAIA 1360
 GR6.SEO
 GRVERS. SEQ TACAAAGGCTCTCAAGTCGCACCAGCCCGAACTGGAACAAAA 1360
 GRVER4. SEQ TAICAAAGGCTCTCAAGTICGCCCCAGCCCGAACTIGGAAGAAA 1360
 GRVER3. SEO TAICIA A IA GGCTCTC A IA GTICIG CICIC CIA GCTIGA A CTIGIGA A GAIAIA 1360
 GRVER2. SEQ TATAA A A G G C T C T C A A G T C G C C C A G C T G A G C T G G A A G A A A 1360
 GRVER1.SEQ TATAAAGGCTCTCAGGTCGCCCCAGCTGAGCTGAAGAAGA 1360
 YG81-6G1.SEOT ATAAGGGCTCTCAGGTAGCACCTGCAGAACTAGAAGAGA 1360
 RDVER1.SEO TACAAGGGTAGCCAAGTGGCTCCTGCCGAATTGGAGGAAA 1360
 RDVER2.SEO TAICIA A GGGIT A GCICAIAIGTIGIG CITIC CTGCICIG A AITITIGIG A GIGA GA 1360
 RDVER3.SEQ TACAAGGGTAGCCAGGTGGCTCCAGCCGAGTTGGGAGGAGA 1360
 RDVER4.SEQ TACAAGGGTAGCCAGGTTGCCTCCAGCTTGAGTTGGGAGGAGA 1360
 RDVERS. SEO TAICIA A GGGIT A GCIC A GGTITIG CITIC CIAIG CITIG AIG TITIGIG AIGIG A G A 1360
          TAICHAGGGTAGCCAGGTTGCTCCHAGCTGAGTTGGGAGGAGA 1360
 RDVER51.SEO TAICIA A GGGITA GCICA GGTITIGCITIC CIAIGCITIGAIGTITIGIGAIGIGA GA 1360
 RDVER52.SEO TAICIA A GGGITA GCICA GGTITIGCITIC CIAIGCITIGAIGTITIGIGA A GA 1360
 RD1561H9.SEQT ACAAGGGTAGCCAGGTTGCTCCAGCTGAGTTGGAGGAGAGA 1360
GRVER51.SEQ T T T T G C T G A A G A A C C C T T G T A T C C G C G A C G T G G C C G T C G T 1400
         TTTTIG CITG A AIGIA AICIC CITITG TA TCICIGIGIG AICIG TIGIG CICIG TICIG T 1400
GRVERS.SEQ TTTTGCTGAAGAACCCTTGTATCCGCGGGTGGCCGTCGTTGT 1400
GRVER4.SEQ TTTTGCTGAAGAACCCTTTGTATCCGGCGACGTGGCCGTCGTT400
GRVER3.SEQ TTTTGCTGAAGAACCCTTGTATTCGCGGACGTGGCCGTCGT 1400
GRVER2.SEQ TETTGCTGAAGAACCCTTTGCATTCGTGACGTGGCCGTCGT 1400
GRVERI.SEQ TCTTGCTGAAGAACCCTTTGCATTCGTGACGTGGCCGTCGT 1400
YG81-6G1.SEO TITTATIGAAAAATCCATGTATCAGAGATGTTGCTGTGGT 1400
RDVERLSEO TICTGTTGAAAAATCCATGTATCCGCGATGTCGCTGTGGT 1400
RDVER2.SEQ TTCTGTTGAAAAATCCATGTATCCGGCGATGTCGCTGTGGT 1400
RDVER3.SEQ TTCTGTTGAAAATCCATGCATCCGTGATGTCGCTGTTGT 1400
RDVER4.SEQ TTCTGTTGAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
RDVER5.SEO TICTGTTGAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
          TTICITIGITT GAAAATC CATGICIATIT CIGICIGAT GTICIG CT GT G GT 1400
RD7.SEO
RDVER51.SEQ TTCTGTTGAAAATCCATGCATTCGGGATGTCGCTGTTGT 1400
RDVER52.SEQ TTCTGTTGAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
RD1561H9.SEQ TTCTGTTGAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
GRVER51.SEQ GGGTATCCCAGACTTGGAAGCTGGCGAGTTGCCTAGCGCC1440
GR6.SEQ
          GIG G T A TICIC CIAIG AIC TITIGIG A A G C T G GICIG AIG TIT G C CIT A G CIG C CI 1440
GRVER5.SEQ GGGTATCCCAGACTTGGGAAGCTGGCGAGTTGCCTAGCGCC1440
         GGGTATCCCAGACTTGGAAGCTGGTGAGTTGCCTAGCGCC1440
 GRVER4.SEO
 GRVER3.SEQ GGGTATCCCAGACTTGGAAGTTGGAAGTTGCCTAGCGCC1440
 GRVER2.SEO GGGTATICIC CIAGATITIGGAAGCTGGCGAGCTGCCITAGCGCCI1440
 GRVER1.SEQ GGGTATCCCCAGATTTGGAAGCTGGCGAGCTGCCTAGCGCC 1440
 YG81-6G1.SEOT G G T A T T C C T G A T C T A G A A G C T G G A G A A C T G C C A T C T G C G 1440
 RDVER1.SEQ CG GCATTCCTGACCTGGAGGCCGGTGAATTGCCATCTGCT 1440
 RDVER2.SEQ CGGCATTCCTGACCTGGAGGCCGGTGAATTGCCATCTGCT 1440
 RDVER3.SEO CG GCATTCCTGATCTGGAGGCCGGTGAACTGCCTTCTGCTT 1440
 RDVER4.SEQ CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCT 1440
 C G G C A T T C C T G A T C T G G A G G C C G G C G A A C T G C C T T C T G C T 1440
 RDVER51.SEQ C G G C A T T C C T G A T C T G G A G G C C G G C G A A C T G C C T T C T G C T 1440
RDVER52.SEQ C G G C A T T C C T G A T C T G G A G G C C G G C G A A C T G C C T T C T G C T 1440
 RD1561H9. SEQCGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCT 1440
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FIG. 2 (cont'd)

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GRVER5.SEQ TTTGTGGT|G|AAACA|A|CCCGG|C|AAGGAGAT|C|AC|T|GCTAA|GG 1480
 GRVER4.SEQ TTTGTGGTGAAACAACCTGGAAAGGAGATCACTGCTAAGG 1480
 GRVER3.SEQ TTTGTGGTGAAACAACCTGGCAAGGAGTTACTGCTAAGG 1480
 GRVER2.SEQ TTTGTCGTGAAACAACCAGGCAAGGAAATTACCGCTAAAG 1480
 GRVER1.SEQ TITGTCGTGAAACAACCAGGTAAGGAAATTACCGCTAAAG 1480
 YG81-6G1.SEOTTTGTGGTTAAACAGCCCGGAAAGGAGTTACAGCTAAAG 1480
 RDVER1.SEQ TTCGTGGTCAAGCAGCCTGGCAAAGAGAGATCACTGCCAAGG 1480
 RDVERZ.SEQ TTCGTGGTCAAGCAGCCTGGTAAAGAGAGATCACTGCCAAGG 1480
 RDVER3.SEQ TTCGTCGTCAAGCAGCCTGGTAAAGAAATCACCGCCAAAG 1480
 RDVER4.SEQ TTCGTTGTCAAGCAGCCTGGTAAAGAAATTACCGCCAAAG 1480
 RDVERS.SEQ TTCGTTGTCAAGCAGCCTGGTAAAGAATTACCGCCAAAG 1480
 RD7. SEQ TTCGTTGTCAAGCAGCCTGGTAAAGAAATTACCGCCAAAG 1480
 RDVER51.SEQ TTCGTTGTCAAGCAGCCTGGTAAAGAATTACCGCCAAAG 1480
 RDVER52. SEQ T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G 1480
 RD1561H9.SEQT T C G T T G T C A A G C A G C C T G G T A C A G A A A T T A C C G C C A A A G 1480
GRVER51.SEQ AGG TOT A C G ACT A TITGG C C G A GOGG G TGT CT C AC A C C A A 1520
GR6.SEQ
           AGG TICTACGAICTATITIGG C C G A GICIGIG TIGT CITICACIA CICIA A 1520
GRVER5.SEQ
          AGGTCTACGACTATTTGGCCGAGCGCGTGTCTCACACCAA 1520
GRVER4.SEQ AGG TICT ACGAICT AT TTTGGCCGAGCGGTGTCTCTCAICAC LA 1520
GRVER3.SEQ AGGTCTACGAICT AT TTTGGCCGAGCGCGTGTCTCACACTAA 1520
GRVER2.SEQ AGG TICT A CG ACT A TITTGG C CG AGCGCG TGT CTC ACA CTA A 1520
GRVER1.SEQ AGGTCTACGACTATTTGGCCGAACGCGTGTCTCACACTAA 1520
YG81-6G1.SEQ AAGTGTACGATTATCTTGCCGAGAGGGTCTCCCATACAAA 1520
RDVER1.SEQ AAGTGTATGATTACCTGGCTGAGCGTGTCAGCCATACCAA 1520
RDVER2.SEQ
          AAGTGTAITGATTAICICTIGIGCITIGAACIGITIGTCAGICCATACICAA 1520
RDVER3.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G A G C C A T A C C A A 1520
RDVER4.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520
RDVER5.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520
RD7.SEQ
          AAGTGTATGATTACCTGGCTGAACGTGTGAGCCATACTAA 1520
RDVER51.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520
RDVER52.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520
RD1561H9.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520
GRVER51.SEQ ATATCTGCGTGGCGGGGGGTCCGCTTCGTCGATTCTATTCCA 1560
GR6.SEO
          ATATCTGCGTGGCGGCGTCCGCTTCGTCGATTCTATTCA 1560
GRVER5.SEO
          ATATICT G C G T G G C G G C G T C C G C T T C G T C G A T T C T A T T C C A 1560
 GRVER4.SEO
          ATATCTGCGTGGCGGCGTCCGCTTCGTCGATTCCATCCAA1560
 GRVER3. SEQ ATATCTGCGTGGCGTCGGCTTCGTCGATTCTATCCCT 1560
 GRVER2.SEQ GTACCTGCGTGGCGGTGTCCGCTTCGTCGATAGCATCCCT 1560
 GRVER1.SEQ GTACCTGCCTGGCGGTGTCCCCTTCCGTGGATAGCATCCCT 1560
 YG81-6G1. SEQG T A T T T G C G T G G A G G G T T C G A T T C G T T G A T A G C A T A C C A 1560
 RDVER1.SEQ ATATTTGCGCGGTGGCGTGCGTTTTGTCGACTCTATTCCA 1560
 RDVER2.SEQ ATATTTGCGCGGGGGGGGCGTGCGTTTTGGTGGACTCTATTCCA 1560
 RDVER3.SEQ GTACTTGCGTGGCGTGCGTTTTTGTGGACAGCATTCCA 1560
 RDVER4.SEQ GTACTTGCGTGGCGTGCGTTTTTGTGGATAGCATTCCT 1560
 RDVERS.SEQ GTACTTGCGTGGCGGCGTGCGTTTTTGTTGACTCCATCCCT 1560
          GTACTTGCGTGGCGGCGTGCGTTTTTGTTGACTCCATCCCT 1560
 RDVER51.SEQ GTACTTGCGTGGCGGCGTGCGTTTTTGTTGACTCCATCCCTT1560
RDVER52.SEQ GTACTTGCGTGGCGGCGTGCGTTTTTGTTGACTCCATCCCTT1560
 RD1561H9.SEQGTACTTGCGTGGCGGCGTTTTTTGTTGACTCCATCCCTT1560
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FIG. 2 (cont'd)

GRVER51. SEQ CGCAACGTTAC CGGTAAGATCACTCGTAAAGAGTTGCTG	A 1600
GR6.SEQ CGCAACGTTACCGGTAAGATCACTCGTAAAGAGTTGCTG	A 1600
GRVER5.SEQ CGCAACGTTACCGGTAAGATCACTCGTAAAGAAGTTGCTG	A 1600
GRVER4.SEQ CGCAACGTGACCGGTAAGATCACTCGTAAAGAATTGCTG	
GRVER3.SEQ CGCAACGTCACCGGCAAGATCACTCGTAAAAGAGTTGCTG	A 1600
GRVER2.SEQ CGCAATGTCACCGGCAAAATTACTCGTAAGGAGTTGCTG	
GRVER1.SEQ CGCAATGTCACCGGCAAAATTACTCGTAAGGAGTTGCTG	A 1600
YG81-6G1. SEQAGGAATGTTACAGGTAAAATTACAAGAAAGGAACTTCTG	
RDVER1.SEQ CGTAACGTGACTGGTAAGATCACCCGCAAAGAACTGTTG	A 1600
RDVER2.SEQ CGTAACGTGACTGGTAAGATCACCCGCAAAGAACTGTTG	A 1600
RDVER3.SEQ CGTAATGTGACTGGTAAAATTACCCGCAAGGAACTGTTG	
RDVER4.SEQ CGCAATGTGACTGGCAAAATTACCCGCAAGGAGCTGTTG	A 1600
RDVER5.SEQ CGTAACGTAACAGGCAAAATTACCCGCAAAGGAGCTGTTG	A 1600
RD7.SEQ CGTAACGTAACAGGCAAAATTACCCGGCAAGGAGCTGTTG	
RDVER51.SEQ CGTAACGTAACAGGCAAAATTACCCGCAAAGGAGCTGTTG	
RDVER52.SEQ CGTAACGTAACAGGCAAAATTACCCGCAAAGGAGCTGTTG	
RD1561H9.SEQCGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTG	1600
GRVER51.SEQ A G C A A C T C C T C G A A A A A G C T G G C G G C	1626
GR6.SEQ AGCAACTCCTCGAAAAAGCTGGCGGC	1626 1626
GRESEQ AGCAACTCCTCGAAAAAGCTGGCGGCGCGREERSSEQAGCAACTCCTCGAAAAAGCTGGCGGC	1626 1626
GRÁSEQ A GCA A CITÓC TICGA Á A A A A GCITÓGGGGGGGGRARASSEQ A GCA A CITÓGA CITÓGA A A A A GCITÓGGCGCGCGRAEASEQ A GCA A CITÓGA A A A A A GCITÓGCGGCGGCGA CITÓGGA A A A A A GCITÓGCG GC	1626 1626 1626
GR6.SEQ A G C A A C T C C T C G A A A A A A G C T G G C G G C GRVER4.SEQ A G C A A C T C C T C G A A A A A A G C T G G C G G C GRVER4.SEQ A G C A A C T C C T C G A A A A A G C T G G C G G C GRVER3.SEQ A A C A A T T G C T C C G A A A A A B G C T G G C G G C	1626 1626 1626 1626
GRÉSEQ A CA A CITIC TIC 6 A A A A A CITIG G G G G G G GRVERSEQ A CA A CITIC CITIG G A A A A G CITIG G G G G G G G G G G G G G G G G G G	1626 1626 1626 1626 1626
GRÁSEQ A G C A A C T C C T C G A A A A A A G C T G G C G G C GRVERASEQ A G C A A C T C C T C G A A A A A A G C T G G C G G C GRVERASEQ A G C A A C T C C T C G A A A A A A G C T G G C G G C GRVERASEQ A A C A A T T G C T C G A A A A A G G C T G G C G G C GRVERASEQ A A C A G T T G C T G G A A A A G G C T G G T G G C GRVERASEQ A A C A G T T G C T G G A A A A G G C T G G T G G C GRVERASEQ A A C A G T T G C T G G A A A A G G C T G G T G G C	1626 1626 1626 1626 1626 1626
GR6.SEQ A G C A A C T C C T C G A A A A A A G C T G G C G G C GRVER4.SEQ A G C A A C T C C T C G A A A A A A G C T G G C G G C GRVER4.SEQ A G C A A C T C C T C G A A A A A A G C T G G C G G C GRVER4.SEQ A A C A A T T G C T C G A A A A A A G C C T G G C G G C GRVER2.SEQ A A C A G T T G C T G G A A A A A G G C T G G T G G C G C GRVER1.SEQ A A C A G T T G C T G G A A A A G G C T G G T G G C Y G G A G G C G G G G G G G G G G G G G G	1626 1626 1626 1626 1626 1626 1626
GRSEQ A G C A A C T C C T C G A A A A A G C T G G C G G C GRVERASSEQ A G C A A C T C C T C G A A A A A G C T G G C G G C GRVERASEQ A C C A C T C C C G A A A A A A G C T G G C G G C GRVERASEQ A A C A G T T G C T C G A A A A A A G C T G G C G G C GRVERASEQ A A C A G T T G C T G G A A A A G G C T G G T G G C G G C GRVERASEQ A A C A G T T G C T G G A A A A G G C T G G T G G C G C C	1626 1626 1626 1626 1626 1626 1626
GRASEQ A G C A A C T C C T C G A A A A A A G C T G G C G G C GRVERASEQ A C C A A C T C C T C G A A A A A A G C T G G C G G C GRVERASEQ A C C A A C T C C T C G A A A A A A A G C T G G C G G C GRVERASEQ A A C A A T T G C T C G A A A A A A A G C T G G C G G C GRVERASEQ A A C A A C T T G C T G G A A A A A A G C T G G T G G C GRVERASEQ A A C A G T T G C T G G A A A A A G C C T G G T G G C GRVERASEQ A C C A G T T G C T G G A G A A A G G C T G G T G G C YGSI-GGLSEQ A C C A G T T G C T G G A G A A A G G C C G G C G G C RDVERLSEQ A C C A G T T G C T T G G A G A A A A G C C G G C G G T RDVERLSEQ A C C A A C T G T T G G A G A A A A G C C G G C G G T	1626 1626 1626 1626 1626 1626 1626 1626
GRÉSEQ A G C A A CIT C C T C G A A A A A A G C T G G C G G C GRVERASSEQ A G C A A CIT C C T C G A A A A A A G C T G G C G G C G G C GRVERASEQ A G C A A CIT C C T C G A A A A A A G C T G G C G G C GRVERASEQ A A C A G T G C T G G C G A A A A A A G C T G G C G G C GRVERASEQ A A C A G T T G C T G G A A A A A G C T G G T G G C G G C GRVERASEQ A A C A G T T G C T G G A A A A G G C T G G T G G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G C G G C G G C G G C G G C G G C G G C G G C G G C G G C C G C C G C C G C C G C C G C	1626 1626 1626 1626 1626 1626 1626 1626
GRÁSEQ A G C A A C T C C T C G A A A A A G C T G G C G G C GRVERASEQ A C C A A C T C C T C G A A A A A G C T G G C G G C GRVERASEQ A C C A A C T C C T C G A A A A A A G C T G G C G G C GRVERASEQ A C C A A C T C C T C G A A A A A A G C C T G G C G G C GRVERASEQ A C A G T T G C T G G A A A A A G G C T G G C G G C GRVERASEQ A C A G T T G C T G G A A A A G G C T G G T G G T G G C GRVERASEQ A C C A G T T G C T G G A C A A G G C T G G T G T G G T G G T G G T G G T G G T G G T G G T G G T G T G G T G G T G T G G T G T G G T G T G G T G T G G T G T G T G T G G T G T G T G T G T G T G T G T G T G T G T G T G T G T G T G T G G T G	1626 1626 1626 1626 1626 1626 1626 1626
GRÉSEQ A CA A CIT C CT C G A A A A A G CT G G G G G G GRVERSEQ A CA A CIT C CT C G A A A A G CT G G C G G C GRVERSEQ A CA A CIT C CT C G A A A A G CT G G C G G C GRVERSEQ A CA A CIT C CT C G A A A A A G CT G G C G G C GRVERSEQ A CA CAT G CT G G C G G C GRVERSEQ A A CA A G CT G G C G C G C G G C GRVERSEQ A A C G CT G C G C G C G G C G G C G G C G G C G G C C G C C C C C C C C C C C C C C C C C C C C	1626 1626 1626 1626 1626 1626 1626 1626
GRSEQ A C C A C T C C T C G A A A A A G C T G G C G G C GRVERASSEQ A C C A A C T C C T C G A A A A A G C T G G C G G C G C GRVERASSEQ A C C A C T C C T C G A A A A A G C T G G C G G C G G C GRVERASSEQ A C C A C T C C T C G A A A A A A G C T G G C G G C G G C GRVERASSEQ A C C G T G C T G G C G A C A A C T G C C G G C G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G C G G C G G C G G C G G C G G C G C G C G C G G C G G C G G C G G C G G C	1626 1626 1626 1626 1626 1626 1626 1626
GRSEQ	1626 1626 1626 1626 1626 1626 1626 1626
GRSEQ A C C A C T C C T C G A A A A A G C T G G C G G C GRVERASSEQ A C C A A C T C C T C G A A A A A G C T G G C G G C G C GRVERASSEQ A C C A C T C C T C G A A A A A G C T G G C G G C G G C GRVERASSEQ A C C A C T C C T C G A A A A A A G C T G G C G G C G G C GRVERASSEQ A C C G T G C T G G C G A C A A C T G C C G G C G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G G C G C G G C G G C G G C G G C G G C G C G C G C G G C G G C G G C G G C G G C	1626 1626 1626 1626 1626 1626 1626 1626

FIG. 2 (cont'd)

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GRVER51.SEO MMKREKN VIVGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
       MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPOA 118
GR6.SEQ
GRVER5.SEQ MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPOA 118
GRVER4.SEQ MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPOA 118
GRVER3.SEO MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPOA 118
GRVER2.SEQ MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPOA 118
GRVER1.SEQ MMKREKNVIYGPEPLHPLEPLTAGEMLFRALRKHSHLPOA 118
YG81-6G1.SEQM M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P O A 118
RDVER1.SEO MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPOA 118
RDVER2.SEO MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
RDVER3.SEQ MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPOA 118
RDVER4.SEQ MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
RDVERS.SEQ MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
        MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSYLPQA 118
RD7.SEQ
RDVER51.SEQ MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
RDVER52.SEQ MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
RD1561H9.SEOMIKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
GRUER 51. SEO I. V D V V G D E S I. S Y K E F F E A T V L L A O S L H N C G Y K M N D V V S I C 238
GR6.SEQ LVDVVGDENLSYKEFFEATVLLAQSLHNCGYKMNDVVSIC 238
GRVERS.SEQ LVDVVGDESLSYKEFFEATVLLAQSLHNCGYKMNDVVSIC 238
GRVER4.SEQ LVDVVGDESLSYKEFFEATVLLAQSLHNCGYKMNDVVSIC 238
GRVER3.SEQ LVDVVGDESLSYKEFFEATVLLAQSLHNCGYKMNDVVSIC 238
GRVER2.SEO LVDVVGDESLSYKEFFEATVLLAOSLHNCGYKMNDVVSIC 238
GRVER1.SEQ LVDVVGDESLSYKEFFEATVLLAQSLHNCGYKMNDVVSIC 238
YGRI-GGI.SEOL V D V V G D E S L S Y K E F F E A T V L L A O S L H N C G Y K M N D V V S I C 238
RDVER1.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RDVER2.SEQ LVDVVGDESLSYKEFFEATVLLAQSLHNCGYKMNDVVSIC 238
RDVER3.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RDVFR4.SEO L V D V V G D E S L S Y K E F F E A T V L L A O S L H N C G Y K M N D V V S I C 238
RDVER5.SEQ L V D V V G-D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RD7.SEO
         LVDVVGDESLSYKEFFEATVLLAOSLHNCGYKMNDVVSIC 238
RDVER51.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RDVER52.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RD1561H9.SEQL V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
GRVER51.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
         AENNTREFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
GR6.SEO
GRVER5.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
GRVER4.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
GRVER3.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
GRVER2.SEO AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
GRVER1.SEO AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
YG81-6G1.SEQAENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
RDVER1.SEO A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
RDVER2.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
RDVER3.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
RDVER4.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
RDVER5.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
         AENNTREFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
RD7.SEQ
RDVER51.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
RDVER52.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
RD1561H9.SEQAENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
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GRVERS1. SEO K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
       KPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
GR6.SEO
GRVERS. SEQ K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
GRVER4.SEQ KPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
GRVER3.SEQ KPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
GRVER2.SEQ KPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
GRVER1.SEQ KPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
YG81-6G1.SEQKPQIVFTTKNILNKVLEVQSRTNFIKRIILDTVENIHGC 478
RDVER1.SEQ KPQIVFTTKNILNKVLEVQSRTNFIKRIILDTVENIHGC 478
RDVER2.SEQ KPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
RDVER3.SEQ KPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
RDVER4.SEO K P Q I V F T T K N I L N K V L E V O S R T N F I K R I I I L D T V E N I H G C 478
RDVER5.SEQ KPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
      K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RDVER51.SEQ K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RDVER52.SEQ K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RD1561H9.SEQKPQIVFTTKNILNKVLEVQSRTNFIKRIILDTVENIHGC 478
GRVER51. SEQ E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
       ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
GR6.SEQ
GRVER5.SEQ ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
GRVER4.SEQ ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
GRVER3.SEO E SLPN FISRY SDGNIAN FKPLH FDPVE QVAAILCS SGTTG 598
GRVER2.SEQ ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
GRVERISEO ESLPNFISRYSDGNIANFKPLHFDPVEOVAAILCSSGTTG 598
YG81-6G1.SEO ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
RDVER1.SEQ ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
RDVER2.SEO E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RDVER3.SEQ ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
RDVER4.SEQ ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
RDVERS.SEO ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
       ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
RD7.SEC
RDVER51.SEQ E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RDVER52.SEQ E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RD1561H9.SEQESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
GRVER51.SEQ LPKGVMQTHQNICVRLIHALDPRVVGTQLIPGVTVLVYLPF 718
       LPKGVMQTHQNICVRLIHALDPRVGTQLISGVTVLVYLPF 718
GRVERS.SEQ LPKGVMQTHQNICVRLIHALDPR|V|GTQLIPGVTVLVYLPF 718
GRVER4.SEQ LPKGVMQTHQNICVRLIHALDPR|V|GTQLIPGVTVLVYLPF 718
GRVER3. SEO LPKGVMQTHQNICVRLIHALDPR|V|GTQLIPGVTVLVYLPF 718
GRVER2. SEQ LPKGVMQTHQNICVRLIHALDPR|V|GTQLIPGVTVLVYLPF 718
GRVER1.SEQ LPKGVMQTHQNICVRLIHALDPRVGTQLIPGVTVLVYLPF 718
YG81-6G1.SEOLPKGVMQTHQNICVRLIHALDPRAGTQLIPGVTVLVYLPF 718
RDVER1.SEQ LPKGVMQTHQNICVRLIHALDPRYGTQLIPGVTVLVYLPF 718
RDVER2.SEQ LPKGVMQTHQNICVRLIHALDPR|Y|GTQLIPGVTVLVYLPF 718
RDVER3.SEQ LPKGVMQTHQNICVRLIHALDPR|Y|GTQLIPGVTVLVYLPF 718
RDVER4.SEQ LPKGVMQTHQNICVRLIHALDPR|Y|GTQLIPGVTVLVYLPF 718
RDVER5.SEQ LPKGVMQTHQNICVRLIHALDPR|Y|GTQLIPGVTVLVYLPF 718
      LPKGVMQTHQNICVRLIHALDPR|Y|GTQLIPGVTVLVYLPF 718
RDVER51.SEQ LPKGVMQTHQNICVRLIHALDPR|Y|GTQLIPGVTVLVYLPF 718
RDVER52.SEO LPKGVMQTHQNICVRLIHALDPR|Y|GTQLIPGVTVLVYLPF 718
RD1561H9.SEQLPKGVMQTHQNICVRLIHALDPRYGTQLIPGVTVLVYLPF 718
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FIG. 3 (cont'd)

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GRVERS1. SEO FHAFGFSITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
        FHAFGFSITLGYFMVGLRVIMFRRFDQEAFLKAIODYEVR 838
GR6.SEO
GRVER5.SEQ FHAFGFSITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
GRVER4.SEQ FHAFGFSITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
GRVER3.SEQ FHAFGFSITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
GRVER2.SEQ FHAFGFSITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
GRVER1.SEO FHAFGFSITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
YG81-6G1.SEOFHAFGFSITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
RDVER1.SEO FHAFGFHITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
RDVER2.SEQ FHAFGFHITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
RDVER3.SEQ FHAFGF|H|ITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
RDVER4.SEO FHAFGFHITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
RDVER5.SEQ FHAFGFHITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
        FHAFGFHITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
RD7 SEO
RDVER51.SEQ FHAFGFHITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
RDVER52.SEO FHAFGFHITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
RD1561H9.SEOFHAFGF|H|ITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
GRVER51.SEO SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
       S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
GR6.SEO
GRVERS.SEQ SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
GRVER4.SEQ SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
GRVER3.SEQ SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
GRVER2.SEQ SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
GRVER1.SEQ SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
YG81-6G1.SEQS V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RDVER1.SEQ SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
RDVER2.SEQ SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
RDVER3.SEO SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
RDVER4.SEO SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
RDVERS.SEO SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
        SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
RDVER51.SEO S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RDVER52.SEO SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
RD1561H9.SEOSVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
GRVER51.SEQ AEVAAKRLNLPGIRCGFGLTESTSANIHSLRDEFKSGSLG 1078
        AEVAAKRLNLPGIRCGFGLTESTSANIHSLRDEFKSGSLG 1078
GRVER5.SEQ AEVAAKRLNLPGIRCGFGLTESTSANIHSLRDEFKSGSLG 1078
GRVER4.SEQ AEVAAKRLNLPGIRCGFGLTESTSANIHSLRDEFKSGSLG 1078
GRVER3.SEQ AEVAAKRLNLPGIRCGFGLTESTSANIHSLRDEFKSGSLG 1078
GRVER2.SEQ AEVAAKRLNLPGIRCGFGLTESTSANIHSLRDEFKSGSLG 1078
GRVER1.SEQ AEVAAKRLNLPGIRCGFGLTESTSANIHSLRDEFKSGSLG 1078
YG81-6G1.SEQAEVAAKRLNLPGIRCGFGLTESTSANIHSLRDEFKSGSLG 1078
RDVER1.SEO A E VAAKRINIPGIRCGFGITESTSATITOSIRDEFKSGSIG 1078
RDVER2.SEO AEVAAKRLNLPGIRCGFGLTESTSA|I|I|Q|SLRDEFKSGSLG 1078
RDVER3.SEQ AEVAAKRINIPGIRCGFGLTESTSA|I|I|Q|SLRDEFKSGSLG 1078
RDVER4.SEQ AEVAAKRLNLPGIRCGFGLTESTSA|I|I|Q|SLRDEFKSGSLG 1078
RDVERS.SEO A E V A A K R L N L P G I R C G F G L T E S T S A I I I O S L R D E F K S G S L G 1078
        AEVAAKRINIPGIRCGFGLTESTSAIIIQSLRDEFKSGSLG 1078
RDVER51.SEO A E V A A K R L N L P G I R C G F G L T E S T S A I I Q S L R D E F K S G S L G 1078
RDVER52.SEQ A E V A A K R L N L P G I R C G F G L T E S T S A I I I Q S L G D E F K S G S L G 1078
RD1561H9.SEQAEVAAKRLNLPGIRCGFGLTESTSALIIQTLGDEFKSGSLG 1078
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FIG. 3 (cont'd)

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GRVER51. SEO R V T P L M A A K I A D R E T G K A L G P N O V G E L C I K G P M V S K G Y V N 1198
         RVTPLMAAKIADRETGKALGPNOVGELCIKGPMVSKGYVN 1198
GRVERS.SEO RVTPLMAAKIADRETGKALGPNOVGELCIKGPMVSKGYVN 1198
GRVER4.SEO RVTPLMAAKIADRETGKALGPNOVGELCIKGPMVSKGYVN 1198
GRVER3.SEO R V T P L M A A K I A D R E T G K A L G P N O V G E L C I K G P M V S K G Y V N 1198
GRVER2.SEQ RVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGYVN 1198
GRVER1.SEQ RVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGY.VN 1198
YG81-6G1.SEOR V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RDVER1.SEO R V T P L M A A K I A D R E T G K A L G P N O V G E L C I K G P M V S K G Y V N 1198
RDVER2.SEO R V T P L M A A K I A D R E T G K A L G P N O V G E L C I K G P M V S K G Y V N 1198
RDVER3.SEO R V T P L M A A K I A D R E T G K A L G P N O V G E L C I K G P M V S K G Y V N 1198
RDVER4.SEO R V T P L M A A K I A D R E T G K A L G P N O V G E L C I K G P M V S K G Y V N 1198
RDVER5. SEO R V T P L M A A K I A D R E T G K A L G P N O V G E L C I K G P M V S K G Y V N 1198
         RVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGYVN 1198
RDVER51.SEQ R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RDVER52.SEO R V T P L M A A K I A D R E T G K A L G P N O V G E L C I K G P M V S K G Y V N 1198
RD1561H9.SEOR V T P L M A A K I A D R E T G K A L G P N O V G E L C I K G P M V S K G Y V N 1198
GRVER51.SEO N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
GR6.SEO
         N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
GRVER5.SEO NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318
GRVER4.SEO NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318
GRVER3.SEO NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318
GRVER2.SEQ NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318
GRVERI.SEO NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELTK 1318
YG81-6G1.SEQN V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RDVERLSEO NVEATKEATDDDGWLHSGDFGYYDEDEHFYVVDRYKELTK 1318
RDVER2.SEQ NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318
RDVER3.SEQ NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318
RDVER4.SEQ NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318
RDVER5.SEQ NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318
RD7.SEO
        NVEATKEAT D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L T K 1318
RDVER51.SEQ N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RDVER52.SEO N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RD1561H9.SEON V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
GRVER51.SEO YKGSOVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
         YKGSOVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
GRVER5.SEO YKGSOVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
GRVER4.SEO YKGSOVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
GRVER3.SEQ YKGSQVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
GRVER2.SEO YKGSOVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
GRVER1.SEQ YKGSQVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
YGR1-6G1.SEOY K G S O V A P A E L E E T I. I. K N P C T R D V A V V G T P D I. E A G E I. P S A 1438
RDVER1.SEQ YKGSQVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
RDVER2.SEQ YKGSQVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
RDVER3.SEO YKGSOVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
RDVER4.SEO YKGSOVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
RDVER5.SEO YKGSOVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
         YKGSOVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
RDVER51.SEQ YKGSQVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
ROVER52. SEO Y K G S O V A P A E L E E T L T: K N P C T R D V A V V G T P D T E A G E T P S A 1438
RD1561H9.SEQYKGSQVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
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FIG. 3 (cont'd)

GRVER51.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	1558
GR6.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	1558
GRVER5.SEQ FVVKQPGKEITAKEVYDYLAERVSHTKYLRGGVRFVDSIP	1558
GRVER4.SEQ FVVKQPGKEITAKEVYDYLAERVSHTKYLRGGVRFVDSIP	1558
GRVER3.SEQ FVVKQPGKEITAKEVYDYLAERVSHTKYLRGGVRFVDSIP	1558
GRVER2.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	
GRVER1.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	
YG81-6G1.SEQFVVKQPGKEITAKEVYDYLAERVSHTKYLRGGVRFVDSIP	1558
RDVER1.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	1558
RDVER2.SEQ FVVKQPGKEITAKEVYDYLAERVSHTKYLRGGVRFVDSIP	1558
RDVER3.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	
RDVER4.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	
RDVER5.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	
RD7.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	
RDVER51.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	
RDVER52.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P	
RD1561H9.SEQFVVKQPGTEITAKEVYDYLAERVSHTKYLRGGVRFVDSIP	1558
GRVER51.SEQ R N V T G K I T R K E L L K Q L L E K A G G	1624
GR6.SEQ RNVTGKITRKELLKQLLEKAGG	1624
GRVER5.SEQ RNVTGKITRKELLKQLLEKAGG	1624
GRVER4.SEQ RNVTGKITRKELLKQLLEKAGG	1624
GRVER3.SEQ RNVTGKITRKELLKQLLEKAGG	1624
GRVER2.SEQ RNVTGKITRKELLKQLLEKAGG	1624
GRVER1.SEQ RNVTGKITRKELLKQLLEKAGG	1624
YG81-6G1.SEQ RNVTGKITRKELLKQLLEKAGG	1624
RDVER1.SEQ RNVTGKITRKELLKQLLEKAGG	1624
RDVER2.SEQ RNVTGKITRKELLKQLLEKAGG	1624
RDVER3.SEQ RNVTGKITRKELLKQLLEKAGG	1624
RDVER4.SEQ RNVTGKITRKELLKQLLEKAGG	1624
RDVER5.SEQ RNVTGKITRKELLKQLLEKAGG	1624
RD7.SEQ RNVTGKITRKELLKQLLEKAGG	1624
RDVER51.SEQ RNVTGKITRKELLKQLLEKAGG	1624
RDVER52.SEO RNVTGKITRKELLKOLLEKAGG	1624
RD1561H9.SEQ RNVTGKITRKELLKQLLVKAGG	1624

FIG. 3 (cont'd)

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RELLUC. SEQ ATGACTTCGAAAGTTTATGATCCAGAACAAAGGAAACGGAAACGGA 40
RLUCVER1. SEQAT GGCTT CCA AGGTGT ACG ACC CCG AGC AGCGCA AGCGCA 40
RELLUC. SEQ TGATAACTGGTCCGCAGTGGTGGGCCAGATGTAAACAAAT 80
RLUCVER1. SEQT GATCACCGGCCCTCAGTGGTGGGCCCGCTGCAAGCAGAT 80
RLUCVER2. SEQT GAT CACT GGGC CTC AGT GGT GGGCT CGCT GCAAGCAAAT 80
RLUCFINL. SEQT GATICACT GGGC CTC AGT GGT GGGCT CGCT GCAAGCAAAT 80
RELLUC. SEQ GAATGTTCTTGATTCATTTATTATTATTATGATTCAGAA 120
RLUCVER1.SEQGAACGTGCTGGACTCCTTCATCAACTACTACGACAGCGAG 120
RLUCVER2. SEQ G A A C G T G C T G G A C T C C T T C A T C A A C T A T G A T T C C G A G 120
RLUCFINL. SEQGAACGTGCTGGACTCCTTCATCAACTACTATGATTCCGAG 120
RELLUC. SEQ AAACATG CAGAAAATG CT GTT ATTTTTTTA CATG GT AACG 160
RLUCVER1. SEQN AGC ACG CCG AGA ACG CCG TGA TCT TC CTGC ACG GCA A C G 160
RELLUC. SEQ CGGCCTCTTCTTATTTATGGCGACATGTTGTGCCACATAT 200
REDCVERT . SEQ CCC G C C T CC A G C T A C C T G T G G A G G C A C G T G G T G C C T C A C A T 200
RLUCVER2. SEQCITIG C C T C C A G C T A C C T G T G G A G G C A C G T C G T G C C T C A C A T 200
RIUCFINL. SECCTGCCTCCAGCTACCTGTGGAGGCACGTCGTGCCTCACAT 200
RELLUC. SEQ TGAGCCAGTAGCGCGGTGTATTATACCAGATCTTATTGGT 240
REJUCYERI. SEQUE A G C CEG TEG CEC CET GEN TENTE CETE A CE TE A TEG CE 240
RLUCFINL. SECCGAGCCCGTGGCTAGATGCATCCCTGATCTGATCGGA 240
RELLUC. SEQ ATGGGCAAATCAGGCAAATCTGGTAATGGTTCTTATAGGT 280
RLUCVER1. SEQATGGGCAAGTCCGGCAAGAGCGGCAACGGCTCCTACCGCC 280
RLUCVER2. SEQATGGGTAAGTCCGGCAAGAGGGGAATGGCTCATATCGCC280
RLUCFINL. SEQAT GGGTAAGT CCGGCAAGAGCGGGAAT GGCT CATATCGC C 280
RELLUC. SEQ TACTTGATCATTACAAATATCTTACTGCATGGTTTGAACT 320
RLUCVER1. SEQTGC TGG ACC ACT ACAAGT ACCTGACCGCCT GGTTCG AGCT 320
RLUCVER2.SEQT C C T G G A T C A C T A C A A G T A C C T C A C C G C T T G G T T C G A G C T 320
RLUCFINL. SEQT CCTGG AT CACTACAAGT ACCTCACCGCTTGGTTCGAGCT 320
RELLUC. SEQ TCTTAATTTACCAAAGAAGATCATTTTTTGTCGGCCATGAT 360
RLUCVER1. SEQGC TGA ACCTGC CCA AGA AGA TCA TCT TCG TGGGC CACGAC 360
RLUCVER2. SEQGCTGAACCTTCCAAAGAAAATCATCTTTGTGGGCCACGAC360
RLUCFINL. SEQGC TGA ACCTTC CAAAGAAAT CATCTTTGTGGGGCCACGAC 360
RELLUC. SEQ TGGGGTGCTTGTTTGGCATTTCATTATAGCTATGAGCATC 400
RLUCVER1. SEQT G G G G A G C C T G C C T G G C C T T C C A C T A C T C C T A C G A G C A C C 400
RLUCVER2. SEQT G G G G G C T T G T C T G G C C T T T C A C T A C T C C T A C G A G C A C C 400
RLUCFINL. SEQT G G G G G G C T T G T C T G G C C T T T C A C T A C T C T A C G A G C A C C 400
RELLUC. SEQ AAGATAAGAT CAAAGCAATAGTTCACGCTGAAAGTGTAGT 440
RLUCVER1. SEQ AGG ACA AGATCA AGG CCATCG TGC ACG CCG AGA GCG TGG T 440
RLUCVER2. SEQA A G A C A A G A T C A A G G C C A T C G T C C A T G C T G A G A G T G T C G T 440
RLUCFINL. SEQA A G A C A A G A T C A A G G C C A T C G T C C A T G C T G A G A G T G T C G T 440
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RELLUC. SEQ AGATGTGATTGAATCATGGGATGAATGGCCTGATATTGAA 480
  RLUCVER1. SEQUE G A C G T G A T C G A G T C C T G G G A C G A G T G G C C T G A C A T C G A G 480
  RLUCVER2. SEQGG A C G T G A T C G A G T C C T G G G A C G A G T G G C C T G A C A T C G A G 480
  RLUCFINL. SEOG G A C G T G A T C G A G T C C T G G G A C G A G T G G C C T G A C A T C G A G 480
  RELLUC. SEQ GAAGATATTGCGTTGATCAAATCTGAAGGAAGAAAAAA 520
  RLUCVER1.SEQG AGG ACATCG CCCTG ATCAAGAG CGAGG AGG GCG AGAAGA 520
  RLUCVER2. SEQGAGGATATCGCCCTGATCAAGAGCGAAGAGGGGCGAGAAAA 520
  RELLUC. SEQ TGGTTTTGGAGAATAACTTCTTCGTGGAAACCATGTTGCC 560
  RLUCVER1.SEQTGGTGCTGGAGAACAACTTCTTCGTGGAGACCATGCTGCC 560
  RLUCVER2. SEQT G G T G C TT G A G A A T A A C T T C T T C G T C G A G A C C A T G C T C C C 560
  RLUCFINL. SEQT G G T G C T T G A G A A T A A C T T C T T C G T C G A G A C C A T G C T C C C 560
  RELLUC. SEQ ATCAAAATCATGAGAAAGTTAGAACCAGAAGAATTTGCA 600
  RLUCVER1.SEQC A G C A A G A T C A T G C G C A A G C T G G G G C T G A G G A G T T C G C C 600
  RLUCYER2.SEDAAGCAAGATCATGCGGAAACTGGAGCCTGAGGAGTTCGCT 600
RLUCFINL.SEQAAGCAAGATCATGCGGAAACTGGAGCCTGAGGAGTTCGCT 600
RELLUC.SEQ GCATATCTTGAACCATTCAAAGAGAAAGGTGAAGTTCGTC 640
RLUCVERISEQ G CCT ACCTGGAGC CCTTCAAGGAGAGAAGGGCGAGGTGCGCC 640
RLUCVER2.SEQ G C C T A C C T G G A G C C C T T C A A G G A G A A G G C G A G G T T A G A C 640
RLUCFINL.SEQ G C C T A C C T G G A G C C A T T C A A G G A G A A G G C C A G G T T A G A C 640
RELLUC.SEQ GTCCAACATTATCATGGCCTCGTGAAATCCCGTTAGTAAA 680
RLUCVERI.SEO GCC CTA CCCTGT CCT G G C CCC GCG AGAT C C CT CTGG T GA A 680
RLUCVER2.SEQ GGC CITA CC CTCT CCT GGCCT CGCGAGATCCCTTCGTTAA 680
RLUCFINL SEO GIGC CITA CCCITCIT CICT GGCCT CGCGAGATCCCITCITCIGTTA A 680
RELLUCISEO
             AGGTGGTAAACCTGACGTTGTACAAATTGTTAGGAATTAT 720
RLUCVERI.SEQ GG GCG GCA AGC CCG A C G TGG TGC AGA TCG TG CGGA AICT AC 720
RLUCVER2.SEQ G G G A G G C A A G C C C G A C G T C G T C C A G A T T G T C C G C A A C T A C 720
RLUCFINL.SEO GG GAG GCA AGC CICGA CGTCG TCC AGATTGTCCGCA ACTAC 720
             AATGCTTATCTACGTGCAAGTGATTATCCAAAAATGT 760
RELLUCISEO
RELUCVERLSEQ AACG COTACCT TO COCCE COLOR GOOGAC CATCT TO COTTA AGAT GT 760
RLUCVERLSEQ AACG COTACCT TC GGG CCA GCGAC GATCT GC CTAAGAT GT 760
RLUCFINLSEO AACG CCTACCT TC GGG CCA GCGAC GATCT GC CTAAGAT GT 760
   RELLUC.SEQ TTATTGAATCGGATCCAGGATTCTTTTCCAATGCTATTGT 800
  RLUCVERL. SEQTICIA TICIG AGT CICIG ACIC CTIG GICT TOTTOTO CA ACIG COATOG T 800
  RLUCYER2.SEQT C A T C G A G T C C G A C C C T G G G T T C T T T T C C A A C G C T A T T G T 800
RLUCFINL.SEQT C A T C G A G T C C G A C C C T G G G T T C T T T T C C A A C G C T A T T G T 800
  RELLUC. SEQ TGAAGGCGCCAAGAAGTTTCCTAATACTGAATTGTCAAA 840
  RLUCVER1. SEQCIG AGG GAG C C A A G A A G T TCC C CA ACA C C G AGT TCG TGA AG 840
  RLUCVER2.SEQCGAGGGAGCTAAGAATTCCCTAACACCGAGTTCGTGAAG 840
  RLUCFINL. SECCIGAGG GAG CITA A GAAGT TICC CTAAICA CICGAGT TICG TIGAAG 840
   RELLUC. SEQ GTAAAAGGTCTTCATTTTTCGCAAGAAGATGCACCTGATG 880
  RLUCVERL. SEQG TGA AGG GCC TGC ACT TCT CCC AGG AGG ACG CCC CTG ACG 880
   RLUCFINL. SEQ G TIGIA A IGIG GICIC TICIC A ICIT TIC A G CIC A IGIG A IGIG A ICIG CITIC CIAIG A T G 880
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FIG. 7 (cont'd)

RELLUC. SEQ A A A T G G G A A A A T A T A T C A A A T C G T T C G T T G A G C G A G T T C T RUCCERI. SEQ A G C G G G T G A G C A A G G A G C G A G C T C G T G G A G C G C G T G C T RUCCERI. SEQ A A A T G G G T A A G T A C A T C A T C G T T C G T G G A G C G C G T G C T RUCCERI. SEQ A A A T G G G T A A G T A C A T C A T C G T T C G T G G A G C G C G T G C T RUCCERI. SEQ A A T G G G T A A G T A C A T C A T C A T C G T G G A G C G C G T G C T C G T G C T C G T G G A G C G C G T G C T C G T G G A G C G C G T G C T C G T G G A G C G C G T G C T	920
RELLUC.SEQ CAAAATGAACA RLUCVER1.SEQGAAGAACGAGCAG RLUCVER2.SEQGAAGAACAGCAGCAG RLUCTINL.SEQGAAGAACGAGCAG RLUCTINL.SEQGAAGAACGAAGCAG	933 933 933 933

FIG. 7 (cont'd)

			_	_	_																					_															
	RELLUC.SEQ																																								
	RLUCVER1.SEC																																								
	RLUCVER2.SEC																																								
	RLUCFINL. SEC	M	A	s	K	V	Y	D	P	Ε	Q	R	K	R	М	Ι	Т	G	P	Q	W	W	A	R	С	K	Q	M	N '	<i>7</i> I	D	s	F	Ι	N	Y	Y	D	S	Ε	118
	RELLUC.SEQ	ĸ	Н	Α	E	N	А	v	I	F	L	Н	G	N	Α	А	s	s	Y	L	W	R	Н	v	v	P	Н	I	E:	P V	A	R	С	I	I	P	D	L	I	G	238
	RLUCVER1.SEC	K	Н	Α	E	N	Α	٧	Ι	F	L	Н	G	N	Α	Α	s	s	Y	L	W	R	Н	٧	٧	P	Н	Ι	E :	P V	A	R	С	Ι	Ι	P	D	L	Ι	G	238
	RLUCVER2.SEC	K	Н	Α	Ε	N	Α	٧	Ι	F	L	Н	G	N	Α	Α	S	s	Υ	L	W	R	Н	٧	٧	P	Н	Ι	Ε :	P V	A	R	С	Ι	Ι	P	D	L	Ι	G	238
	RLUCFINL. SEC	K	Н	A	Ε	N	A	V	Ι	F	L	Н	G	N	A	A	S	s	Y	L	W	R	Н	V	V	P	Н	Ι	Ε:	? V	A	R	С	Ι	Ι	P	D	L	Ι	G	238
	RELLUC.SEQ	M	G	K	s	G	K	s	G	N	G	s	Y	R	L	L	D	н	Y	K	Y	L	т	A	w	F	Е	L	L	۱ I	P	K	K	I	I	F	v	G	Н	D	358
	RLUCVER1.SEC	M	G	K	s	G	K	S	G	N	G	s	Y	R	L	L	D	Н	Y	K	Y	L	т	Α	W	F	Ε	L	L	1 I	P	K	K	Ι	Ι	F	٧	G	Н	D	358
	RLUCVER2.SEC	M	G	K	S	G	K	S	G	N	G	s	Y	R	L	L	D	Н	Y	K	Y	L	т	Α	W	F	Ε	L	L	N I	P	K	K	Ι	Ι	F	v	G	Н	D	358
	RLUCFINL. SEC	М	G	K	S	G	K	S	G	N	G	S	Y	R	L	L	D	Н	Y	K	Y	L	T	A	W	F	Ε	L	L	1	. P	K	K	Ι	Ι	F	V	G	H	D	358
	RELLUC.SEQ	W	G	Α	С	L	Α	F	н	Y	s	Y	E	н	Q	D	K	I	K	A	I	v	н	Α	E	s	٧	٧	D١	<i>,</i> I	E	s	W	D	Е	W	P	D	I	E	478
	RLUCVER1.SEC	W	G	Α	С	L	Α	F	Н	Y	s	Y	E	Н	Q	D	K	Ι	K	Α	Ι	V	Н	Α	Ε	s	٧	V	D '	<i>1</i>	Ε	s	W	D	E	W	P	D	Ι	E	478
	RLUCVER2.SEC	W	G	Α	С	L	Α	F	Н	Y	s	Y	E	Н	Q	D	K	Ι	K	Α	Ι	V	Н	Α	Ε	s	٧	V	D '	<i>1</i>	Ε	s	W	D	Ε	W	P	D	Ι	E	478
	RLUCFINL. SEC	W	G	A	С	L	A	F	Н	Y	s	Y	Ε	Н	Q	D	K	Ι	K	A	Ι	V	Н	A	E	s	V	V	D 1	/ I	Е	S	W	D	Ε	W	P	D	Ι	E	478
	LLUC.SEQ																																								598
	UCVER1.SEQ																																								
	UCVER2.SEQ																																								
RL	UCFINL.SEQ	Ε	D	Ι	A	L	Ι	K	s	Ε	Ε	G	Ε	K	M	V	L	Ε	N	N	F	F	٧	E	Т	M	L	P	S I	(I	M	R	K	L	Ε	P	Ε	Ε	F	A	598
	LLUC.SEQ																																								718
	UCVER1.SEQ																																								
	UCVER2.SEQ																																								
RI.	UCFINL.SEQ	A	Y	L	Ε	P	F	K	Ε	K	G	Ε	V	R	R	P	Т	L	S	W	P	R	Ε	Ι	P	L	٧	K	G	; K	P	D	٧	V	Q	Ι	V	R	N	Y	718
	LLUC.SEQ																																								838
	UCVER1.SEQ																																								
	UCVER2.SEQ																																								
RI.	UCFINL.SEQ	N	A	Y	L	R	A	S	D	D	L	P	K	M	F	Ι	Ε	S	D	P	G	F	F	s	N	A	I	V :	E	A	K	K	F	P	N	T	E	F	V	K	838
																															Q										931
RL	UCVER1.SEQ	v	K	G	L	Н	F	s	Q	Ε	D	Α	P	D	E	M	G	K	Y	Ι	K	s	F	v	Ε	R	V	L	K	E	Q										931
RL	UCVER2.SEQ	v	K	G	L	Н	F	s	Q	Ε	D	Α	P	D	Е	M	G	K	Y	Ι	ĸ	s	F	v	Ε	R	v	L	K	E	Q										931
RL	UCFINL.SEQ	v	K	G	L	Н	F	s	Q	Ε	D	Α	P	D	Е	M	G	K	Y	Ι	K	s	F	v	Ε	R	٧	L	K	E	Q										931

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GRVER51. SEQ ATGATGAAACGCGAAAAGAACGTGATCTACGGCCCAGAAC 40
   LUCPPLYG. SEQATGATGAAGAGAGAGAAAAATGTTATATGGACCCGAAC 40
   RD1561H9.SEQATGATAAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGC 40
   GRVER51. SEO CACTGC ATIC CACTGG A A GA CCITCA CCIG CTIG GTIG AGATGCT 80
   LUCPPLYG. SEQCCCTACACCCCTTGGAAGACTTAACAGCAGGAGAAATGCT 80
   RD1561H9.SEQCTCTCCATCCTTTGGAGGATTTGACTGCCGGCGAAATGCT80
   GRVER51. SEQ CTTCCGGAG CACTGCGTA A A CATAGTCACCTCCCTC AAGCA 120
   LUCPPLYG. SEQCTTCAGGGCCCTTCGAAAACATTCTCATTTACCGCAGGCT 120
   RD1561H9.SEQGT TT CGTG CTC TCC GCA AGC ACT C T C A T T TGC CTC AAG CC 120
   GRYERS1. SEO CITCIG TIGIG ACIG TICIGTIGIG GAIG A C. G. AIG A. G. C. T. C. T. A. C. A. A. G. 160
   LUCPPLYG. SEQTTAGTAGATGTGTTTGGTGACGAATCGCTTTCCTATAAAG 160
   RD1561H9.SEQT TGG TCGATGTGGTCGGCGATGAATCTTTGAGCTACAAGG 160
   GRVER51.SEQ AATTTTTCGAAGCTACTGTGCTGTTGGCCCCAAAGCCTCCA 200
   LUCPPLYG. SEQ A G T T T T T T G A A G C T A C A T G C C T C C T A G C G C A A A G T C T C C A 200
   RD1561H9. SEQA G T T T T T T G AGG CAA CCG T CTTGC TGG CTC AG T C C C T C C A 200
GRVER51.SEO TAATTGTGGGTACAAAATGAACGATGTGGTGAGCATTTTGT 240
LUCPPLYG.SEO CAATTGTGGATACAAGATGAATGTAGTGTCGATCTGC 240
RD1561H9.SEO CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGT 240
GRVER51.SEQ GCTGAGAATAACACTCGCTTCTTTATTCCTGTAATCGCTG 280
LUCPPLYG.SEO GCCGAGAATAATAAAAGATTTTTTTATTCCCATTATTGCAG 280
RD1561H9.SEQ GCTGAAAACAATACCCGTTTCTTCATTCCAGTCATCGCCG 280
GRVER51.SEO
           CTTGGTACATCGGCATGATTGTCGCCCCTGTGAATGAATC 320
LUCPPLYG.SEQ CTTGGTATATTGGTATGATTGTAGCACCTGTTAATGAAAG 320
GRVER51.SEQ TTACATCCCAGATGAGCTGTGTGAAGGTTATGGGTATTAGC 360
LUCPPLYG.SEQ ITTACATCCCAGATGAACTCTGTAAGGTCATGGGTATATCG 360
RD1561H9.SEQ ICTACATTCCCGACGAACTGTGTAAAAGTCATGGGTATCTCT I 360
GRVERSLSEO AAACCTICAAATGGTCTTTTACTACGAAAAACATGTTGAATA 400
LUCPPLYG.SEO A A A C C A C A A A T A G T T T T T T G T A C A A A G A A C A T T T T A A A T A 400
RDIS6H9.SEO A AGC CACAGATTG TOTTCACCACTAAGAATATTCTGAACA 400
   GRVER51. SEQ AGGTCTTGGAAGTCCAGTCTCGTACTAACTTCATCAAACG 440
   LUCPPLYG. SEQAGGTATTGGAGGTACAGAGCAGAACTAATTTCATAAAAA 440
   RD1561H9. SEQAAG TCCT G G AAG TCC AAA G CCGCA CCA ACT TTA TTA AG CG 440
   GRVER51. SEQ CATCATTATTCTGGATACCGTCGAAAACATCCACGGCTGT 480
   LUCPPLYG. SEQG ATCATCATACTTGATACTGTAGAAAACATACACGGTTGT 480
   RD1561H9. SECTATCATCATCTTGGACACTGTGGAGAATATTCACGGTTGC 480
   GRVER51. SEO GAGAGCCTCCCTAACTTCATCTCTCGTTACAGCGATGGTA 520
   LUCPPLYG. SEQGAAAGTCTTCCCAATTTTATTTCTCGTTATTCGGATGGAA 520
   RD1561H9. SEQG A AT CITTIGC CTA A TIT TCA TOTOTOTO GOT A TICAG ACG GOA 520
  GRVER51.SEQ AT ATCG CTA ATT T CAAGC CCT TGC AT TT TG AT C CAG TCG A 560
   LUCPPLYG. SEQATATTGCCAACTTCAAACCTTTACATTACGATCCTGTTGA 560
   RD1561H9. SEQACATCG CAAACTTTAAACCACTCCACTTCGACCCTGTGGA 560
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GRVER51. SEQ G C A A G T G G C A G C T A T T T T T G T G C T C C G G C A C C A C T G G T 600
   LUCPPLYG. SEQG CAAGTGGCAGCTATCTTATGTTCGTCAGGCACTACTGGA 600
   RD1561H9.SEQACAAGTTGCAGCCATTCTGTGTAGCAGCGGTACTACTGGA 600
   GRVER51.SEQ T TGC CTAAAGGTGTCATGCAGACTCACCAGAATATCTGTG 640
   LUCPPLYG. SEQTTACCGAAAGGTGTAATGCAAACTCACCAAAATATTTGTG 640
   RD1561H9.SEQCTCC CAA AGG GAG TOA TG CAGA COCATCAA A ACATTTGOG 640
   GRVER51.SEQ TGCGTTTGATCCACGCTCTCGACCCTCGTGTGGGTACTCA 680
   LUCPPLYG. SEQT C C G A C T T A T A C A T G C T T T A G A C C C C A G G G C A G G A A C G C A 680
   RD1561H9.SEQTGCGTCTGATCCATGCTCTCGATCCACGCTACGGCACTCA 680
   GRVER51. SEO ATTGATCCCTGGCGTGACTGTGCTGGTGTATCTGCCTTTC 720
   LUCPPLYG. SEQACTTATTCCTGGTGTGACAGTCTTAGTATATCTGCCTTTT 720
   RD1561H9. SEGGCTGATTCCTGGTGTCACCGTCTTGGTCTACTTGCCTTTC720
   GRVER51.SEQ TITC ACCCCTTTGGTTTCTCTATTACCCTGGGCTATTTCA 760
   LUCPPLYG. SEQTTCCATGCTTTTGGGTTCTCTATAAACTTGGGATACTTCA 760
   RD1561H9.SEQTTCCATGCTTTCGGCCTTTCATATTACTTTGGGTTACTTTA 760
   GRVER51. SEQ T G G T C G G C T T G C G T G T C A T C A T G T T T C G T C G C T T C G A C C A 800
   LUCPPLYG. SEQTGGTGGGTCTTCGTGTTATCATGTTAAGACGATTTGATCA 800
   RD1561H9. SEQT G G T C G C G C G T G A T T A T G T T C G G C G T T T T G A T C A 800
GRVER51.SEO
            A G A A G CCT T C TT G A A G G C T A T T C A A G A CT A C G A G G T G C G T 840
LUCPPLYG.SEQ AGAAGCATTTCTAAAAGCTATTCAGGATTATGAAGTTCGA 840
            GGAGGCTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGC 840
RD1561H9.SEO
            TCCGTGATCAACGTCCCTTCAGTCATTTTGTTCCTGAGCA 880
GRVER51.SEQ
LUCPPLYG.SEO AGTGTAATTAACGTTCCAGCAATAATATTGTTCTTATCGA 880
RD1561H9.SEQ
            AGTGTCATCAACGTGCCTAGCGTGATCCTGTTTTTGTCTA 880
GRVER51.SEO
            A AT CIT C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G 920
LUCPPLYG.SEQ AAAGTCCTTTGGTTGACAAATACGATTTATCAAGTTTAAG 920
RD1561H9.SEO
            AGAGCCCACTCGTGGACAAGTACGACTTGTCTTCACTGCG 920
GRVER51.SEO
            TIG AG CIT GIT GET GET GET GET CETT TGG CCAAAGAAGTG 960
LUCPPLYG.SEQ GGAATTGTGTTGCGGTGCGGCACCATTAGCAAAAGAAGTT 960
RD1561H9.SEQ TGAATTGTGTTGCGGTGCGCTCCACTGGCTAAGGAGGTC 960
   GRUERS 1. SEO G CCG A G G T CG CT G CT A A G C G T CT G A A CCT CC CT G G T A T C C 1000
   LUCPPLYG. SEQG C T G A G G T T G C A G T A A A A C G A T T A A A C T T G C C A G G A A T T C 1000
   RD1561H9. SEQG CT G A A GT GG C C G C C A A A C G C T T G A A T C T T C C A G G G A T T C 1000
   GRVER51.SEO G C T GCG GTT T T G G T T T G A CTG A G A G C A C T T CTG C T A ACA T 1040
   LUCPPLYG. SEOG C T G T G G A T T T G G T T T G A C A G A A T C T A C T T C A G C T A A T A T 1040
   RD1561H9. SEQGET T G T G GCCT TCG GCCT TCA CCG A A T C T A CCA G T G CGATT A T 1040
   GRVER51. SEQ CC ATA GCTTGCGAGACG AGTTTAAGTCTGGTAGCCTGGGT 1080
   LUCPPLYG. SEQACACAGTCTTGGGGATGAATTTAAATCAGGATCACTTGGA 1080
   RD1561H9. SEOCIC AGAICT C TICG G G G A T G AGT T T A A G A G CIG GCT CITTIGG GC 1080
   GRUERS 1. SEQ COCO TO TO TO TO THAT GOOT GOALAGATO COCO ACCOT G 1120
   LUCPPLYG. SEO A G A G T T A C T C C T T T A A T G G C A G C T A A A A T A G C A G A T A G G G 1120
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FIG. 11 (cont'd)

RD1561H9.SEQCGTGTCACTCCACTCATGGCTGCTAAGATCGCTGATCGCG 1120

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GRVER51.SEQ AGACCGGCCAAAGCACTGGGCCCAAATCAAGTCGGTGAATT 1160
LUCPPLYG. SEQAAACTGGTAAAGCATTGGGACCAAATCAAGTTGGTGAATT 1160
RD1561H9.SEQN A A C T G G T A AGG CTT T G G GCC CGA ACC A A G TGG GCG AG CT 1160
GRVER51.SEQ GT GT ATT A AGG G C C CTAT G G T C T A A A G G C T A C G T G A A C 1200
LUCPPLYG. SEQATGCGTTAAAGGTCCCATGGTATCGAAAGGTTACGTGAAC 1200
RD1561H9.SEQGT GT ATCA A A G GCC CTATGGTGAGCAAGGGTT ATGTCA AT 1200
GRVER51. SEQ A A T G TGG AGG CCA CTA A A G A A G CCA T T G A T G A T G G C T 1240
LUCPPLYG. SEQAATGTAGAAGCTACCAAAGAAAGCTATTGATGATGATGATT1240
RD1561H9.SEQA ACG TTG A A G C T A C C A AGG AGG CCA TCG ACG ACG ACG GCT 1240
GRVER51.SEQ GGCTCCATAGCGGCGACTTCGGTTACTATGATGAGGACGA 1280
LUCPPLYG. SEQGGCTTCACTCTGGAGACTTTGGATACTATGATGAGGATGA 1280
RD1561H9.SEQGGTTGCATTCTGGTGATTTTGGATATTACGACGAAGATGA 1280
GRVER51. SEQ ACACTTCTATGTGGTCGATCGCTACAAAGAATTGATTAAG 1320
LUCPPLYG. SEQG CATTTCTATGTGGTGGACCGTTACAAGGAATTGATTAAA 1320
RD1561H9.SEOG CATTTTTTACGTCGTGGATTCGTTACAAGGAGCTGATCAAA 1320
LUCPPLYG. SEQTATAAGGGCTCTCAGGTAGCACCTGCAGAACTAGAAGAGA 1360
RD1561H9.SEQT ACAAGGGTAGCCAGGTTGCTCCAGCTGAGTTGGAGGAGA 1360
GRVER51.SEQ TTTTGCTGAAGAACCCTTGTATCCGCCGACGTGGCCGTCGT 1400
LUCPPLYG. SEQTTTTTATTGAAAAATCCATGTATCAGAGATGTTGCTGTGGT 1400
RD1561H9.SEQTTCTGTTGAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
GRVER51. SEQ GG G T A T C C C A G A C T T GG A A G C T G G C G A G T T G C C T A G C G C C 1440
LUCPPLYG. SEQTGGTATTCCTGATCTAGAAGCTGGAACTGCCATCTGCG 1440
RD1561H9.SEOCIG GCATTCCTGATCTGGAGGCCCGGCCGAACTGCCTTCTGCT 1440
GRVER51. SEO TTTGTGGTGAAACAACCCGGCAAGGAGATCACTGCTAAGG 1480
LUCPPLYG. SEQT T T G T G G T T A A A C A G C C C G G A A A G G A G A T T A C A G C T A A A G 1480
RD1561H9. SEQT TCG TTG TCA AGC AGC CTG GTACAG AAA T T A CCG CCA AA G 1480
GRVER51.SEQ AGG TCT A C G ACT A TTTGG C C G A GCGCG TGT CTC ACA CCA A 1520
LUCPPLYG. SEQAAGTGTACGATTATCTTGCCGAGAGGGTCTCCCATACAAA 1520
RD1561H9. SEQAAGTGTATGATTACCTTGGCTTGAACGTTGTGAGCCATACTAA 1520
GRVER51. SEQ AT A TCT G C G T G GCG GCCG TCC GCT T C G TCCG A TT C T A TTC C A 1560
LUCPPLYG. SEQG T A T T T G C G T G G A G G G G T T C G A T T C G T T G A T A G C A T A C C A 1560
RD1561H9.SEQGTACTTGCGTGGCGGCGTGCGTTTTGTTGACTCCATCCCT 1560
GRVER51. SEQ CGCA ACGTT A CCGGTA AGATCA CTCGTA AAGAGTTGCTGA 1600
LUCPPLYG. SEQAGGAATGTTACAGGTAAAATTACAAGAAAGGAACTTCTGA 1600
RD1561H9.SEQCGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTSTTGA 1600
GRVER51.SEQ AGCAACTCCTCGAAAAAGCTGGCGGC
                                                             1626
LUCPPLYG. SEQAGCAGTTGCTGGAGAAGAGTTCTAAACTT
                                                             1629
RD1561H9. SEQAACAATTGTTGGTGAAGGCCGGCGT
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FIG. 11 (cont'd)

1626

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GRVER51. SEO MMKREKNVIY GPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
   LUCPPLYG.SEOM M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P O A 118
   RD1561H9.SEQMIKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
   GRVER51.SEO LVDVVIG DE SLSYKE FFEATVILLAOSLHNCGYKMNDVVSIC 238
   LUCPPLYG. SEOL V D V F G D E S L S Y K E F F E A T C L L A O S L H N C G Y K M N D V V S I C 238
   RD1561H9.SEOLVD VVG DESLSYKE FFEATVLLAOSLH N C G Y K M N D V V S I C 238
   GRVER51.SEQ AENNTR FFIPVIAAW YIG MIVAPVNES YIP DELCK V M G I S 358
   LUCPPLYG.SEQAENNKRFFIPIIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
   RD1561H9.SEOAENNTR FFIPWIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
   GRVER51.SEO K P O I V FTT K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
   LUCPPLYG. SEOK POIVFCTKNILNKVLEVOSRTNFIKRIIILDTVENIHGC 478
   RD1561H9.SEQKPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
   GRVER51.SEQ E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
   LUCPPLYG. SEQE S L P N F I S R Y S D G N I A N F K P L H Y D P V E Q V A A I L C S S G T T G 598
   RD1561H9.SEOE SLPNFISRYSDGNIANFKPLHFDPVEOVAAILCSSGTTG 598
   GRVER51.SEQ LPKGVMOTHQNICVRLIHALDPRVGTQLIPGVTVLVYLPF 718
   LUCPPLYG. SEQL PKGVMQTHQNICVRLIHALDPRAGTQLIPGVTVLVYLPF 718
   RD1561H9.SEOLPKGVMOTHONICVRLIHALDPRYGTOLIPGVTVLVYLPF 718
GRVER51.SEQ FHAFGFSITLGYFMVGLRVIMFRRFDOEAFLKAIODYEVR 838
LUCPPLYG.SEO FHAFGFSINLGYFMVGLRVIMLRRFDQEAFLKAIQDYEVR 838
RD1561H9.SEO FHAFGFHITLGYFMVGLRVIMFRRFDOEAFLKAIODYEVR 838
GRVER51.SEQ SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
LUCPPLYG.SEO SVINVPAIILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
RD1561H9.SEO SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
GRVER51.SEO A E VA A KRINIPGIR C G F G L T E S T S A N I H S L R D E F K S G S L G 1078
LUCPPLYG.SEO AEVAVKRLNLPGIRCGFGLTESTSANIHSLGDEFKSGSLG 1078
RD1561H9.SEO AEVAAKRINIPGIRCGFGLTESTSATIOTIGDEFKSGSLG 1078
GRVER51.SEO RVTPLMAAKIADRETGKALGPNQVGELCTKGPMVSKGYVN 1198
LUCPPLYC.SEO RVTPLMAAKIADRETGKALGPNOVGELCVKGPMVSKGYVN 1198
RDIS61H9.SEO RVTPLMAAKIADRETGKALGPNQVGELCIIKGPMVSKGYVN 1198
   GRVER51.SEO N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
   LUCPPLYG.SEON V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
   RD1561H9.SEQN V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
   GRVER51.SEO Y K G S O V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
   LUCPPLYG, SEO Y K G S O V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
   RD1561H9.SEQYKGSOVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
   GRVER51.SEO F V V K O P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
   LUCPPLYG. SEO F V V K O P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
   RD1561H9.SEOFVVKOPGTEITAKEVYDYLAERVSHTKYLRGGVRFVDSIP 1558
   GRVER51.SEQ RNVTGKITRKELLKQLLEKAGG
                                                                       1624
   LUCPPLYG. SEOR N V T G K I T R K E L L K Q L L E K S S K L
                                                                       1627
   RD1561H9. SEOR N V T G K I T R K E L L K O L L V K A G G
                                                                       1624
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FIG. 17B

GRver5.1 DNA sequence of pGL3 vectors

ATUGTGAAACGCGAAAAGAACGTGATCTACGGCCCAGAACCACTGCATCC	50
ACTGGAAGACCTCACCGCTGGTGAGATGCTCTTCCGAGCACTGCGTAAAC	100
ATAGTCACCTCCCTCAAGCACTCGTGGACGTCGTGGGAGACGAGAGCCTC	150
TCCTACAAAGAATTTTTCGAAGCTACTGTGCTGTTGGCCCAAAGCCTCCA	200
TAATTGTGGGTACAAAATGAACGATGTGGTGAGCATTTGTGCTGAGAATA	250
ACACTCGCTTCTTTATTCCTGTAATCGCTGCTTGGTACATCGGCATGATT	300
GTCGCCCCTGTGAATGAATCTTACATCCCAGATGAGCTGTGTAAGGTTAT	350
GGGTATTAGCAAACCTCAAATCGTCTTTACTACCAAAAACATCTTGAATA	400
AGGTCTTGGAAGTCCAGTCTCGTACTAACTTCATCAAACGCATCATTATT	450
CTGGATACCGTCGAAAACATCCACGGCTGTGAGAGCCTCCCTAACTTCAT	500
$\tt CTCTCGTTACAGCGATGGTAATATCGCTAATTTCAAGCCCTTGCATTTTG$	550
ATCCAGTCGAGCAAGTGGCCGCTATTTTGTGCTCCTCCGGCACCACTGGT	600
$\tt TTGCCTAAAGGTGTCATGCAGACTCACCAGAATATCTGTGTGCGTTTGAT$	650
CCACGCTCTCGACCCTCGTGTGGGTACTCAATTGATCcCTGGCGTGACTG	700
TGCTGGTGTATCTGCCTTTCTTTCACGCCTTTGGTTTCTCTATTACCCTG	750
$\tt GGCTATTTCATGGTCGGCTTGCGTGTCATCATGTTTCGTCGCTTCGACCA$	800
${\tt AGAAGCCTTCTTGAAGGCTATTCAAGACTACGAGGTGCGTTCCGTGATCA}$	850
ACGTCCCTTCAGTCATTTTGTTCCTGAGCAAATCTCCTTTGGTTGACAAG	900
${\tt TATGATCTGAGCAGCTTGCGTGAGCTGTGCTGTGGCGCTGCTCCTTTGGC}$	950
${\tt CAAAGAAGTGGCCGAGGTCGCTGCTAAGCGTCTGAACCTCCCTGGTATCC}$	1000
GCTGCGGTTTTGGTTTGACTGAGAGCACTTCTGCTAACATCCATAGCTTG	1050
$\tt CGAGACGAGTTTAAGTCTGGTAGCCTGGGTCGCGTGACTCCTCTTATGGC$	1100
TGCAAAGATCGCCGACCGTGAGACCGGCAAAGCACTGGGCCCAAATCAAG	1150
${\tt TCGGTGAATTGTGTATTAAGGGCCCTATGGTCTCTAAAGGCTACGTGAAC}$	1200
AATGTGGAGGCCACTAAAGAAGCCATTGATGATGATGGCTGGC	1250
$\tt CGGCGACTTCGGTTACTATGATGAGGACGAACACTTCTATGTGGTCGATC$	1300
GCTACAAAGAATTGATTAAGTACAAAGGCTCTCAAGTCGCACCAGCCGAA	1350
$\tt CTGGAAGAAATTTTGCTGAAGAACCCTTGTATCCGCGACGTGGCCGTCGT$	1400
GGGTATCCCAGACTTGGAAGCTGGCGAGTTGCCTAGCGCCTTTGTGGTGA	1450
AACAACCCGGCAAGGAGATCACTGCTAAGGAGGTCTACGACTATTTGGCC	1500
${\tt GAGCGCGTGTCTCACACCAAATATCTGCGTGGCGGCGTCCGCTTCGTCGA}$	1550
TTCTATTCCACGCAACGTTACCGGTAAGATCACTCGTAAAGAGTTGCTGA	1600
AGCAACTCCTCGAAAAAGCTGGCGGC	1626

SEQ ID NO: 297

FIG. 18A

RDver5.1 DNA sequence of pGL3 vectors

ATGGTGAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGCCT	CTCCATCC	50
TTTGGAGGATTTGACTGCCGGCGAAATGCTGTTTCGTGCTCTC	CCGCAAGC	100
ACTCTCATTTGCCTCAAGCCTTGGTCGATGTGGTCGGCGATG	AATCTTTG	150
AGCTACAAGGAGTTTTTTGAGGCAACCGTCTTGCTGGCTCAG	ICCCTCCA	200
CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGTGCT	TGAAAACA	250
ATACCCGTTTCTTCATTCCAGTCATCGCCGCATGGTATATCGC	STATGATC	300
GTGGCTCCAGTCAACGAGAGCTACATTCCCGACGAACTGTGTA	AAAGTCAT	350
GGGTATCTCTAAGCCACAGATTGTCTTCACCACTAAGAATATT	TCTGAACA	400
AAGTCCTGGAAGTCCAAAGCCGCACCAACTTTATTAAGCGTAT	CATCATC	450
TTGGACACTGTGGAGAATATTCACGGTTGCGAATCTTTGCCTA	AATTTCAT	500
CTCTCGCTATTCAGACGGCAACATCGCAAACTTTAAACCACTC	CCACTTCG	550
ACCCTGTGGAACAAGTTGCAGCCATTCTGTGTAGCAGCGGTAG	CTACTGGA	600
CTCCCAAAGGGAGTCATGCAGACCCATCAAAACATTTGCGTGG	CGTCTGAT	650
CCATGCTCTCGATCCACGCTACGGCACTCAGCTGATTCCTGGT	FGTCACCG	700
TCTTGGTCTACTTGCCTTTCTTCCATGCTTTCGGCTTTCATAT	TACTTTG	750
GGTTACTTTATGGTCGGTCTCCGCGTGATTATGTTCCGCCGTT	TTGATCA	800
GGAGGCTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGCAGT	IGTCATCA	850
ACGTGCCTAGCGTGATCCTGTTTTTGTCTAAGAGCCCACTCGT	rggacaag	900
TACGACTTGTCTTCACTGCGTGAATTGTGTTGCGGTGCCGCTC	CACTGGC	950
TAAGGAGGTCGCTGAAGTGGCCGCCAAACGCTTGAATCTTCCA	AGGGATTC	1000
GTTGTGGCTTCGGCCTCACCGAATCTACCAGCGCTATTATTCA	AGTCTCTC	1050
CGCGATGAGTTTAAGAGCGGCTCTTTGGGCCGTGTCACTCCAC	TCATGGC	1100
TGCTAAGATCGCTGATCGCGAAACTGGTAAGGCTTTGGGCCCC	BAACCAAG	1150
TGGGCGAGCTGTGTATCAAAGGCCCTATGGTGAGCAAGGGTTA	ATGTCAAT	1200
AACGTTGAAGCTACCAAGGAGGCCATCGACGACGACGGCTGGT	TTGCATTC	1250
TGGTGATTTTGGATATTACGACGAAGATGAGCATTTTTACGTC	CGTGGATC	1300
GTTACAAGGAGCTGATCAAATACAAGGGTAGCCAGGTTGCTCC	CAGCTGAG	1350
TTGGAGGAGATTCTGTTGAAAAATCCATGCATTCGCGATGTCC	CTGTGGT	1400
CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCTTTC	GTTGTCA	1450
AGCAGCCTGGTAAAGAAATTACCGCCAAAGAAGTGTATGATTA	CCTGGCT	1500
GAACGTGTGAGCCATACTAAGTACTTGCGTGGCGGCGTGCGT	TTGTTGA	1550
CTCCATCCCTCGTAACGTAACAGGCAAAATTACCCGCAAGGAG	CTGTTGA	1600
AACAATTGTTGGAGAAGGCCGGCGGT		1626

SEQ ID NO: 299

FIG. 18A (cont'd)

RD1561H9 DNA sequenc of pGL3 vectors

ATGGTAAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGCCTCTCCATCC	50
${\tt TTTGGAGGATTTGACTGCCGGCGAAATGCTGTTTCGTGCTCTCCGCAAGC}$	100
ACTCTCATTTGCCTCAAGCCTTGGTCGATGTGGTCGGCGATGAATCTTTG	150
AGCTACAAGGAGTTTTTTGAGGCAACCGTCTTGCTGGCTCAGTCCCTCCA	200
CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGTGCTGAAAACA	250
ATACCCGTTTCTTCATTCCAGTCATCGCCGCATGGTATATCGGTATGATC	300
GTGGCTCCAGTCAACGAGAGCTACATTCCCGACGAACTGTGTAAAGTCAT	350
GGGTATCTCTAAGCCACAGATTGTCTTCACCACTAAGAATATTCTGAACA	400
AAGTCCTGGAAGTCCAAAGCCGCACCAACTTTATTAAGCGTATCATCATC	450
${\tt TTGGACACTGTGGAGAATATTCACGGTTGCGAATCTTTGCCTAATTTCAT}$	500
CTCTCGCTATTCAGACGGCAACATCGCAAACTTTAAACCACTCCACTTCG	550
ACCCTGTGGAACAAGTTGCAGCCATTCTGTGTAGCAGCGGTACTACTGGA	600
CTCCCAAAGGGAGTCATGCAGACCCATCAAAACATTTGCGTGCG	650
CCATGCTCTCGATCCACGCTACGGCACTCAGCTGATTCCTGGTGTCACCG	700
TCTTGGTCTACTTGCCTTTCTTCCATGCTTTCGGCTTTCATATTACTTTG	750
GGTTACTTTATGGTCGGTCTCCGCGTGATTATGTTCCGCCGTTTTGATCA	800
GGAGGCTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGCAGTGTCATCA	850
ACGTGCCTAGCGTGATCCTGTTTTTGTCTAAGAGCCCACTCGTGGACAAG	900
${\tt TACGACTTGTCTTCACTGCGTGAATTGTGTTGCGGTGCCGCTCCACTGGC}$	950
TAAGGAGGTCGCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC	1000
GTTGTGGCTTCGGCCTCACCGAATCTACCAGTGCGATTATCCAGACTCTC	1050
GGGGATGAGTTTAAGAGCGGCTCTTTGGGCCGTGTCACTCCACTCATGGC	1100
TGCTAAGATCGCTGATCGCGAAACTGGTAAGGCTTTGGGCCCGAACCAAG	1150
TGGGCGAGCTGTGTATCAAAGGCCCTATGGTGAGCAAGGGTTATGTCAAT	1200
AACGTTGAAGCTACCAAGGAGGCCATCGACGACGACGGCTGGTTGCATTC	1250
TGGTGATTTTGGATATTACGACGAAGATGAGCATTTTTACGTCGTGGATC	1300
GTTACAAGGAGCTGATCAAATACAAGGGTAGCCAGGTTGCTCCAGCTGAG	1350
TTGGAGGAGATTCTGTTGAAAAATCCATGCATTCGCGATGTCGCTGTGGT	1400
CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCTTTCGTTGTCA	1450
AGCAGCCTGGTACAGAAATTACCGCCAAAGAAGTGTATGATTACCTGGCT	1500
GAACGTGTGAGCCATACTAAGTACTTGCGTGGCGGCGTGCGT	1550
CTCCATCCCTCGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA	1600
AACAATTGTTGGTGAAGGCCGGCGGT	1626

SEQ ID NO: 301

FIG. 18A (cont'd)

GRver5.1 protein sequence of pGL3 vectors

MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL SYKEFFEATULLAQSLHNCGYKMIDDVSICAENNTRFFIEVIAAWYIGMI VAPVNESYIPDELCKWMGISKPOIVFTKKILIKVLEVGORTNFIKELII LDTVENIHGCESLPHSIGRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG LPKGVMQTHQNICVRLIHALDDRVGTLIGFGTVLUVLPFFHARGFSITL GYFMVGLKVIMFRRFDQBAFLKAIQDVEVRSVINVPSVILFISKSPLVDK YDLSSLRELCGAAPLAKEVAEVAAKRINLPGIRGGFGITBSTSANIHSL RDEFKSGSLGRVTPLMAAKIADRETGKALGPMQVGELCIKGPMYSKGYVN NVBATKERIDDDGWLHSGDFGYYDEDBHFYVVDRYKELIKYKGSQVAPAE LEEILKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGKBITAKEVYDYLA ERVSHTKYLRGGVRFVDSIPRNVTGKITRKELLKQLLEKAGG	150 200 250 300 350 400 450	SEQ ID NO: 298
RDver5.1 protein sequence of pGL3 vectors MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL SYKEFFEATVLLAQSLHNCGYKMRDVVSICAENNTRFFIPVIAAWYIGMI VAPVNESYIPDELCKVMGISKPQIVFTTKNILINKVLEVQSRTNFIRRIII LDTVENIHGCESLPHFISRYSDGNIABFKPLHFDVVEQVAATLCSSGTTG LPKGVMQTHQNICV&LIHALDPRYGTQLIBGVTVLYVLPFFHARGFHTTL GYFMVGLRVJWFRFRDGBAELKAIDDVEWSVINVPSVLIHFLSKSPLVMK VDLSSLRELCCGAAPLAKEVABVAAKKLNLPGIRCGFGLTESTSAIIQSL RDEFKSGSLGRVYPLMAAKIADRETGRAGPGNVGELCKKGPMVSKGVVN NVBATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIKYKGSQVAPAE LEBILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGKBITAKEVYDYLA ERVSHTKYLKGGGVPFVSIF BRNVTGKITRKEKLIKOLLEKAGG	150 200 250 300 350 400 450	SEQ ID NO: 300
RD1561H9 protein sequence of pGL3 vectors MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL SYKEFFEATVLLAGSLENGGYKMMDVVSICAENNTRFIPVIAAWYIGMI	50 100 150 200 250 300 350	SEQ ID NO: 302

FIG. 18A (cont'd)

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NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIKYKGSQVAPAE 450 LEEILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGTEITAKEVYDYLA 500 ERVSHTKYLRGGVRFVDSIPRNVTGKITRKELLKQLLVKAGG